

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:13 ; Search time 95.6613 Seconds
(without alignments)
1091.732 Million cell updates/sec

Title: US-10-056-052A-4
Perfect score: 1732
Sequence: 1 MVAADAPAGTDTITNQLTV.....NGSGSGDGIDKPVPEQPD 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1727	99.7	933	2 Q53653	Q53653 staphylococ
2	1662	96.0	946	16 Q8NXJ1	Q8NXJ1 staphylococ
3	1517	87.6	935	16 Q932C5	Q932C5 staphylococ
4	1517	87.6	989	16 Q99VJ4	Q99VJ4 staphylococ
5	1112	64.2	881	2 Q93MH7	Q93MH7 staphylococ
6	416.5	24.0	961	16 Q99RD3	Q99RD3 staphylococ
7	409	23.6	940	2 Q53682	Q53682 staphylococ
8	393	22.7	943	16 Q8NUU8	Q8NUU8 staphylococ
9	353	20.4	931	2 Q9K113	Q9K113 staphylococ
10	349	20.2	1056	16 Q8CQ72	Q8CQ72 staphylococ
11	349	20.2	1092	2 Q70022	Q70022 staphylococ
12	326.5	18.9	1141	16 Q8NXJ5	Q8NXJ5 staphylococ
13	324.5	18.7	1038	16 Q99RD2	Q99RD2 staphylococ
14	323.5	18.7	1166	2 Q86489	Q86489 staphylococ
15	323	18.6	566	2 Q8KR22	Q8KR22 staphylococ
16	322.5	18.6	1015	16 Q8NUU7	Q8NUU7 staphylococ

17	320.5	18.5	1141	16 Q99W46	Q99W46 staphylococ
18	320.5	18.5	1141	16 Q932F7	Q932F7 staphylococ
19	312.5	18.0	877	16 Q99R07	Q99R07 staphylococ
20	312.5	18.0	913	2 Q86476	Q86476 staphylococ
21	298	17.2	1171	2 Q9KMX6	Q9KMX6 staphylococ
22	291.5	16.8	907	16 Q8NUU0	Q8NUU0 staphylococ
23	257.5	14.9	1315	2 Q86488	Q86488 staphylococ
24	256.5	14.8	1347	16 Q8NXJ6	Q8NXJ6 staphylococ
25	240.5	13.9	1385	16 Q99W47	Q99W47 staphylococ
26	232	13.4	970	16 Q8DY17	Q8DY17 streptococ
27	232	13.4	1310	16 Q8E473	Q8E473 streptococ
28	230.5	13.3	955	16 Q8NXX7	Q8NXX7 staphylococ
29	229.5	13.3	953	16 Q99W48	Q99W48 staphylococ
30	210.5	12.2	947	2 Q86487	Q86487 staphylococ
31	204	11.8	1161	2 Q8RJ10	Q8RJ10 streptococ
32	204	11.8	1161	2 Q9X3M7	Q9X3M7 streptococ
33	201.5	11.6	1633	16 Q8CMP4	Q8CMP4 staphylococ
34	201.5	11.6	1733	2 Q9K114	Q9K114 staphylococ
35	197	11.4	1893	2 Q8KX11	Q8KX11 staphylococ
36	182	10.5	1039	2 P72534	P72534 streptococ
37	182	10.5	1160	2 Q8RM86	Q8RM86 streptococ
38	161.5	9.3	463	16 Q92DD5	Q92DD5 listeria in
39	157.5	9.1	462	16 Q8Y8L7	Q8Y8L7 listeria mo
40	152	8.8	642	16 Q89810	Q89810 clostridium
41	151.5	8.7	3240	16 Q87P85	Q87P85 vibrio para
42	147.5	8.5	586	16 Q92FA3	Q92FA3 listeria in
43	142	8.2	766	2 Q9EXR6	Q9EXR6 bacillus sp
44	141	8.1	1386	16 Q92DL0	Q92DL0 listeria in
45	141	8.1	1681	5 Q81548	Q81548 plasmodium

ALIGNMENTS

RESULT 1

ID Q53653 PRELIMINARY; PRT; 933 AA.

AC Q53653; 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)

DE Clumping factor.

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_Taxid=1280;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Newman;

RX MEDLINE=94224142; PubMed=8170386;

RA McDevitt D., Francois P., Vaudaux P., Foster T.J.;

RT "Molecular characterization of the clumping factor (fibrogen receptor

RT of Staphylococcus aureus.";

RL Mol. Microbiol. 11:237-248 (1994).

CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY

CC AN AMIDE BOND (BY SIMILARITY).

CC EMBL; Z18852; CAA79304.1; -.

DR PIR; S41539; S41539.

DR PDB; 1N67; 04-MAR-03.

DR GO; GO:0005618; C:cell wall; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR000515; BPD_transp.

DR InterPro; IPR001899; Gpos_Y5IRK.

DR InterPro; IPR001899; Gram_pos_anchor.

DR Pfam; PF00746; Gram_pos_anchor; 1.

DR Pfam; PF04650; Y5IRK_signal; 1.

DR	TIGRFAMS; TIGR01167; LpxTG anchor; 1.
DR	PROSITE; PS00402; BPD_TRANS_P INN_MEMBER; 1.
DR	PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
KW	Cell wall; Peptidoglycan-anchor.
SQ	SEQUENCE 933 AA; 97058 MW; EB51A6DE2FF759F4 CRC64;

Query Match 99.7%; Score 1727; DB 2; Length 933;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNQLTNTVTGIDSGTIVYPHQAGYVKLNYSVNSAVKGDTFKITVP 61
DB 221 VAADAPAGTDTITNQLTNTVTGIDSGTIVYPHQAGYVKLNYSVNSAVKGDTFKITVP 280
QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFIDYVNTKDDVKATLTMPAYID 121
DB 281 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFIDYVNTKDDVKATLTMPAYID 340
QY 122 PENVKKTGNVTLATGIGSTTANKTVLVDYEKGFYNLSIKGTIDQIDKTNTYRQITIYV 181
DB 341 PENVKKTGNVTLATGIGSTTANKTVLVDYEKGFYNLSIKGTIDQIDKTNTYRQITIYV 400
QY 182 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKVDNAADLSESYFVNPENFEDVTN 241
DB 401 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKVDNAADLSESYFVNPENFEDVTN 460
QY 242 SVNITFPNPQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDIALRSTLYGYSNIIWRS 301
DB 461 SVNITFPNPQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDIALRSTLYGYSNIIWRS 520
QY 302 MSWDNEVAFNNGSGSGDGIDKPVVEQPD 331
DB 521 MSWDNEVAFNNGSGSGDGIDKPVVEQPD 550

RESULT 2

Q8NXJ1 PRELIMINARY; PRT; 946 AA.
AC Q8NXJ1;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Fibrinogen-binding protein.
GN ClfA OR MM0764.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004824; BAB94629.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000515; BPD_transp.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS00402; BPD_TRANS_P_INN_MEMBER; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Complete proteome.
SQ SEQUENCE 946 AA; 98238 MM; EFFB838793201173 CRC64;

Query Match 96.0%; Score 1662; DB 16; Length 946;
Best Local Similarity 95.8%; Pred. No. 2.1e-84;
Matches 316; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNQLTNTVTGIDSGTIVYPHQAGYVKLNYSVNSAVKGDTFKITVP 61
DB 220 VAADAPAGTDTITNQLTNTVTGIDSGTIVYPHQAGYVKLNYSVNSAVKGDTFKITVP 279

QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFIDYVNTKDDVKATLTMPAYID 121
DB 280 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFIDYVNTKENVTANITMPAYID 339
QY 122 PENVKKTGNVTLATGIGSTTANKTVLVDYEKGFYNLSIKGTIDQIDKTNTYRQITIYV 181
DB 340 PENVKKTGNVTLATGIGSTTANKTVLVDYEKGFYNLSIKGTIDQIDKTNTYRQITIYV 399
QY 182 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKVDNAADLSESYFVNPENFEDVTN 241
DB 400 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKVDNAADLSESYFVNPENFEDVTN 459
QY 242 SVNITFPNPQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDIALRSTLYGYSNIIWRS 301
DB 460 SVNITFPNPQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDIALRSTLYGYSNIIWRS 519
QY 302 MSWDNEVAFNNGSGSGDGIDKPVVEQPD 331
DB 520 MSWDNEVAFNNGSGSGDGIDKPVVEQPD 549

RESULT 3

Q932C5 PRELIMINARY; PRT; 935 AA.
AC Q932C5;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Fibrinogen-binding protein.
GN FNB OR SAV0811.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003360; BAB56973.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000515; BPD_transp.
DR InterPro: IPR005877; Gpos_YsIRK.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR Pfam: PF04650; YsIRK_signal; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS00402; BPD_TRANS_P_INN_MEMBER; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Complete proteome.
SQ SEQUENCE 935 AA; 96950 MM; DC5A2D92CE3BA91C CRC64;

Query Match 87.6%; Score 1517; DB 16; Length 935;
Best Local Similarity 87.3%; Pred. No. 2.4e-76;
Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNQLTNTVTGIDSGTIVYPHQAGYVKLNYSVNSAVKGDTFKITVP 61
DB 221 VAADAPAGTDTITNQLTNTVTGIDSGTIVYPHQAGYVKLNYSVNSAVKGDTFKITVP 280
QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFIDYVNTKDDVKATLTMPAYID 121
DB 281 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFIDYVNTKENVTANITMPAYID 340

QY	122	PENUKKTGNVTLATIGISTTANKTVLVDYEKYGKFYNLSIKGTIDQIDKTNNTTYROTIIYV	181
Dd	341	PENVTKTGNTLTGTGINTASKTVLDIYEEKYGFHNLSIKGTIDQIDKTNNTTYRQTIIYV	400
QY	182	NPSGDNVIAPLVTGNLKPNRTDSNALIDQONTSIKYVKVDNAADLSSESYFVNEDNEFDVTN	241
Dd	401	NPSGDNVVLPALTGNLI PNIXSNALIDAKNTDIKYRVNDANMLSESYYVNBSDFEDEVTN	460
QY	242	SVNITFPNPNOYKVEFNTPDDQITTPYIVVNGHIDPNSKGLALRSTLYGYSNNIIWRS	301
Dd	461	QVRISFPNANOYKVEFPPTDDQITTPYIVVNGHIDPASTGLALRSTFYGYDSNFIIWS	520
QY	302	MSWDNEVAFPNNGSGSGDGIDKPVVPDPE	331
Dd	521	MSWDNEVAFPNNGSGSGDGIDKPVVPDPE	550

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RESULT 4
O99VT4          PRELIMINARY;      PRT;       989 AA.
ID O99VT4
AC O99VT4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
GN Fibrinogen-binding protein A, clumping factor.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Iian J., Ito T., Kanamori M.,
RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL, AP003131; BAB41975.1; -.
DR PIR; D89852; D89852.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005877; GPoS_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor_1.
DR pfam; PF04650; YSIRK_signal; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Complete proteome.
SQ SEQUENCE    989 AA;   102407 MM;   DA6E807539623467 CRC64;

Query Match              87.6%; Score 1517; DB 16; Length 989;
Best Local Similarity    87.3%; Pred. No. 2.6e-76;
Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0

Db        2 VAADAPAAAGTDITNQLTNVTVGIDSGITVYPHQAGYVKLNYGFSVPNSAVKGDTFKITVP 61
|||||
Db        221 VAADAPAAGTDITNQLTVDKVITDTSGLTYPHQAGYVKLNYGFSVPNSAVKGDTFKITVP 280
|||||

QY        62 KELNLNGVTSTAKVPPIMAGDOVLANGVIDSDGNVIYTFTDYNTKDVKATLTMPAYID 121
|||||
DB        281 KEINLVGVSTAKVPPIMAGDOVLANGVIDSDGNVIYTFTDYDNKENVTANTTMPAYID 340
|||||

QY        122 PENVKKTGNVTLATGISGSTTANKVTLVDYEKGKFYNLSIKGTIDQIDKTNNTYROTIVV 181
|||||
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Db      341 PENVTKRGVTLTTGTIGTNTASKVYLIDYEKGQGFHNLISIKGTIDQIDKTNNTYRQTIYV 400

QY      182 NPSGDVYIAPVLGTGNLKPNTDSNALIDQONTSIKVKYKVDNAADLSSESYFVNPNFEDVTN 241
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      401 NPSGDVYVLPALTGNLIPNTKSNALIDAKNTDIKYRVDNANDLSSESYVNPSPDFEDVTN 460

QY      242 SVNITFPNPNQYKVEFNTPPDQITTPYIVVNGHIDPNSKGDIALRSTLYGYSNIIWRS 301
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      461 QVRISFPNANQYKVEFPTDDQITTPYIVVNGHIDPASTGDIALRSTFYGYDSNFIWRS 520

QY      302 MSWDNEVAFNNGSGSGDGDIDKPVVPEQDPE 331
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      521 MSWDNEVAFNNGSGSGDGDIDKPVVPEQDPE 550

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RESULT 5
Q93MH7 PRELIMINARY; PRT; 881 AA.
ID Q93MH7
AC Q93MH7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Receptin Fbl precursor.
GN FBL.
OS Staphylococcus lugdunensis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=28035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2342;
RA Nilsson M., Ahlen J., Frykberg L., Guss B.;
RT "A fibrinogen-binding protein of Staphylococcus lugdunensis.";
RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY AN AMIDE BOND (BY SIMILARITY).
CC EMBL; AF404823; AAK95649.1; -.
DR DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 39 POTENTIAL.
FT CHAIN 40 881 RECEPTIN_FBL.
SQ SEQUENCE 881 AA; 94251 MM; D4296C4959CAF19B CRC64;

Query Match 64.2%; Score 1112; DB 2; Length 881;
Best Local Similarity 62.6%; Pred. No. 7.3e-54;
Matches 201; Conservative 50; Mismatches 70; Indels 0; Gaps 0;

QY 11 TDITNQLNTVTVGIDSGTTVP HQAGYVKLNFGSVPN SAVKGDTFRKITVPKELNLNGVT 70
   :|::||::||| ::|:||||::| ||| |::|::|::|::|
Db 214 SDISNKLSNVATITEADTIYPHKAKEYNLNYRFQAPDDVQAGDSIKITIPQALNLNGVT 273
   :|||:|||||::| |::|:|||||::|::|:|||||::|
QY 71 STAKVPPI MAGDQVLANGVIDSDGVNIYFTDYNTKDV KATLTMPAYIDPEN VKKTGN 130
   :|||:|||||::| |::|:|||||::|::|:|||||::|
Db 274 ATAKAPNIMAGDQILATGTIDEENGLIYFTDYTNKNNTITGQSI PGYIDPKNVHTGK 333
   :|||:|||||::| |::|:|||||::|::|:|||||::|
QY 131 VTLATGISSTANKTVLVLDYEKYGFKNLSIKGTIDQIDKTNNTYRQTIVYNPSGDNVIA 190
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 334 VNLETSGQTAKTAVTVVDYEKGEFFNL SIKGTIDQIDKVNNTYRQTVYVNPSSDTVVD 393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 191 PVLTGNLKENTDSNALIDQNTSIRKYKVYDNAA DLSESYFVNPEPEDVTNSVNI TFPNP 250
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 394 PYLRGGSIPGTNSNVILDEQNTSIRKYKVEKAHL TDSYVVDPSPNEDEVTS DVKITPFPEK 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 251 NQYKVEFTPDQGITTPYIVVVGHI DPNSKGD LALRSTLYGYNSNI IWRSMWDNEVAF 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 454 GIYQINFETEDDQINSPIYVVI NGHVDPSNGNL YLRSTLYGYDSNFTRVSMAMDNEVEY 513

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QY      311  NNGSGSGDGDIDKPVVPEQPDF 331
      :||:|||||:|:|:
Db      514  HAGSGNGDGDIDKPVIPDQPGD 534

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RESULT 6

ID	Q99RD3	PRELIMINARY;	PRT;	961 AA.
AC	Q99RD3;			
DT	01-JUN-2001	(TRMBLrel. 17, Created)		
DT	01-JUN-2001	(TRMBLrel. 17, Last sequence update)		
DT	01-JUN-2003	(TRMBLrel. 24, Last annotation update)		
DE	FnbB protein (Fibronectin-binding protein homolog).			
GN	FNB8 OR SAV2502 OR SA2290.			
OS	Staphylococcus aureus (strain Mu50 / ATCC 700699), and			
OS	Staphylococcus aureus (strain N315).			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=158878, 158879;			

RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Haseyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiramatsu H., Kihara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003365; BAB58664.1; -.
DR EMBL; AP003137; BAB43593.1; -.
DR PIR; G90053; G90053.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Complete proteome.
SQ SEQUENCE 961 AA; 106010 MW; 364940F884EA4101 CRC64;

Query Match	24.0%;	Score 416.5;	DB 16;	Length 961;
Best Local Similarity	29.1%;	Pred. No. 3.8e-15;		
Matches 101; Conservative	69;	Mismatches 144;	Indels 33;	Gaps 9;

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QY      2 VAADAPAACTDITNOLINTVTVGID----SGTTVYPHOAGYVKLNIGFSVPENSAVKGDITFK 57
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     158 VAEAKATGTDVTNKVEVTESSLEGHKNDNSIVNPHNAORVTLKKYKMKFEGEIKAGDYFD 217
QY      58 ITVEKELNLNGVSTSTAKVPPIMAG--DOYLANGVIDSDGNVIYFTFDYVNTKDDYKATLT 115
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     218 FTLSDNVETHGISTLRKVPKIKSSTEDKWMANGQVINERTIRYTFPTDYINNKDOLTAELN 277
QY      116 MPAYIDPENVKKTGNVTLATIGSTTANKTVLDY----EKYGFYNLSIKGTIDQIDK 170
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     278 LNFLDPTVTVKQGSQKVEVTLGQNKVSKEDIKYLDGVKDRMG---VTVNGRIDTLNKK 333
QY      171 TNNTRYQTIYVNPSSGDNVIAVPLTGNLKPNTDSNALIDQONTSIKVYKVDNAADISESYF 230
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     334 EEGKFSHFAYVKPNNSLTSVTVIGQVTSYKQSA---NNPTVKVYKHHIGSDELASVY 389
QY      231 V---NPNFEDVTNSVNI TFPNPNQYKVEFNTPDDQITTPYIVVNGHIDPNSKGLALR 287
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

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D**b** 390 AKLDITSPKEDVTEKANLSYTSNGGYTLNLGDDL--SKDYIKYEGEYDQNAK-DLNR 446
Q**y** 288 STLYGYNSTNIWR-----SMWDNEVAFNNGSGGDIDKPVP 326
 : | ||| : :: | | | | : : | | | | |
D**b** 447 TLHSGYHKIYPYPYPYEVQLTWNNGVAFYSSNAKGDKDKPNP 493

RESULT 7

ID	Q53682	PRELIMINARY;	PRT;	940 AA.
AC	Q53682;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, last annotation update)		
DE	Fibronectin binding protein B.			
GN	FNBB.			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			

```

RP SEQUENCE FROM N.A.
RC STRAIN=8325-4;
RA MEDLINE=92111475; PubMed=1837266;
RX Jonsson K., Signas C., Muller H.P., Lindberg M.;
RT "Two different genes encode fibronectin binding proteins in
RT Staphylococcus aureus. The complete nucleotide sequence and
RT characterization of the second gene.";
RL Eur. J. Biochem. 202;1041-1048(1991).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
CC
DR EMBL; X62992; CAA44726.1; -.
DR PIR; S19702; S19702.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Fn_bind.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 940 AA; 10355 MW; E35FBCA907AE345 CRC64;

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Query Match	23.6%;	Score 409;	DB 2;	Length 940;
Best Local Similarity	28.9%;	Pred. No. 9.7e-15;		
Matches 101;	Conservative 72;	Mismatches 131;	Indels 46;	Gaps 11;

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QY      2 VAADABAAGTDITNÖLTJNTVTGIDSGT-----TVPYHÖAGYVKLNTGFSVENSAY 51
      | : | | | : | : | : | | | | :
Db      155 VVEETKATGTDTVTK-----VEVEHGESEIVGHKÖDTNVVNPNAERVTLLKYYKWKFGEGIK 209
      | : | | | : | : | : | | | | :
QY      52 KGDTFKITVPKELNLTGVTSTAKVYPIMAGD-QVTLANGVIDSDGNVIYTFDQYVNTKDDV 110
      | | | : | : | : | | | | : | | | :
Db      210 AGDYFDFTLSDNVETHGISLTKRVPKSTBDGQVMATGELIGERKVRYTEYQVEKKDL 269
      | | | : | : | : | | | | : | | | :
QY      111 KATLMAYIDPENVKKTGNVTLATGIGSTTANKTVLDY----EKYKGFYNLSIKGTI 165
      | : : | : | : | : | : | : | : | :
Db      270 TAELSLNLFIPTVTÖKGNÖNEVKLGSETTVSKIFENIÖYLGVRDNWG---VTANGRI 325
      | : : | : | : | : | : | : | : | :
QY      166 DÖIDKTNNTRYÖTIYVNPSCGNVIAPLVTGNL---KENPDSNALIDÖÖNTSIIKYKYVDN 221
      | : : | : | : | : | : | : | : | :
Db      326 DTLNKVDGKFSHFAYMKPNÖSLSSVTVTGÖVTKANKPGVN-----NPTVKVYKHIG 377
      | : : | : | : | : | : | : | : | :
QY      222 AADLSESYEVNPNEN---FEDVTNSVNITFPNPNÖKYKEFNTPDÖITTPYIVVNVNGHIDP 278
      | : | : | : | : | | | | : | : | :
Db      378 SDDLAEISYAKLIDVSKFEDVTDNMSLDFDTNGGYSLNFPNNLDDQ--SKNYVIKIEGGYDS 435
      | : | : | : | : | : | : | : | :
QY      279 NSKGDLALRSTLYGYNSNIIMPSMSWDNEVAFNNGSGSGDGIDK---PVV 325

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Db 436 NA-SNLEFQTHLFGYVNYTSLNLTWKNQVAFYSNNAQGDGDKDKLEPIT 484

RESULT 8

Q8NTU8 PRELIMINARY; PRT; 943 AA.
AC Q8NTU8;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE FnbB protein.
GN FNB OR MW2420.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RT Lancet 359:1819-1827(2002).
RL EMBL; AF004830; BAB96285.1;
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Fb bind.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fb_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Complete proteome.
SQ SEQUENCE 943 AA; 104537 MW; DA8A5F31947E1B6A CRC64;

Query Match 22.7%; Score 393; DB 16; Length 943;
Best Local Similarity 29.3%; Pred. No. 7.5e-14;
Matches 103; Conservative 64; Mismatches 141; Indels 44; Gaps 11;

QY 2 VAADAPAAAGTDITNQLNTVTGIDSGT-----TYEPHQAGYVKLNGFSVPNSA 50
Db 155 VVEEAKATGTDVTSK-----VEVEEGSEIVGHNNKETNVNPHNAERVTLKXKMFEDGI 209
QY 51 VKGDPFKITVPKELNLNGVSTAKVPPIMA-GDQVLANGVIDSQNVITYFTDYVNTKDD 109
Db 210 KPGDYFDFTLSNNVETHGISPLRKVPDIKSKDNNILAVGKVMDEKRIRYFTFDYINNNKN 269
QY 110 VKATLMPAYIDPENVKKTGNVTLATIGISTTANKTVLVYD----EKYGKFNLSIKGT 164
Db 270 LMAELNLNLFIDPTVTVKQKQIVBVKLGEMKISKEDIKYLLDGVKDNWG---VTVNGR 325
QY 165 IDQIDKTNNTYRQTIYVNPSCGNVIAVLTGNLKPNTDSNALIDQNTSIVKYKVDNAAD 224
Db 326 ITLLDKENSKIHLAYINPKKSDMTSITINGFFA---KGGIYTGNVPTVKVYEYLRSD 381
QY 225 LSESYFVN--PENFEDVTSVN--ITFPNPQYKVEFNTPDDQITTPYIVVNGHIDPN 279
Db 382 LPESVYANTNDQEKFKDVTNDSMDKLTLSENGSKYKL--TLDALNKKSYVVSFEKYNEN 438
QY 280 SKGDIALRSTLYGYSNIIWR-----SMSWDNEVAFNNGSGSDGIDKPVVP 326
Db 439 DK-ELIFRTNLHGHHANGYIYYPVSLTWDNGVAFYSNNAQGDGDKDPNDP 489

RESULT 9
Q9KI13 PRELIMINARY; PRT; 931 AA.

AC Q9KI13;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Fibrinogen-binding protein sdrG.
GN SDRG.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1282;
RN [1]

RP SEQUENCE FROM N.A.
RX STRAIN=K28;
RX MEDLINE=20340957; PubMed=10878118;
RA McCrea K.W., Hartford O., Davis S., Ni Eidhin D., Lina G.,
RA Speziale P., Foster T.J., Hook M.;
RT "The serine-aspartate repeat (sdr) protein family in Staphylococcus
RT epidermidis.";
RL Microbiology 146:1535-1546(2000).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
DR EMBL; AF245042; AAF72510.1;
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF05738; Cna_B; 2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 931 AA; 102955 MW; 591E657D97027116 CRC64;

Query Match 20.4%; Score 353; DB 2; Length 931;
Best Local Similarity 30.6%; Pred. No. 1.2e-11;
Matches 101; Conservative 60; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLNTVTGI-DSGTTVPHQAGYVKLNGFSVPNSAVKGDTEKITVPKELNLNGVTS 71
Db 285 VTDQ--SITEGYDDSDGIKHAENLIYDVFVEVDKVKSGDWTMTVNIDKNTVPSDLTD 342
QY 72 TAKVPPIMAGD-QVLANGVID-SDGNVIYFTFDYVNTKDDVKATLTMPAYIDPENVKKTG 129
Db 343 SFAIPKIKDNGSEIATGTVDNNKQITTYFTDYVDKVENIKAKLKLTSYIDKSKVPNNN 402
QY 130 --NVTLATIGISTTANKTVLVYDEKYGKFNLSIKGTIDQIDKTNNTYRQTIYVNSGD 186
Db 403 TKLDVEYKTAISS--VNKTIYVEQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPL-- 458
QY 187 NVIAPVLTGNLKPNTDSNALIDQNTSIVKYKVDNAADLSESYFV-NPENFEDVTSVNI 245
Db 459 RYSAKETVNVNISGNDEGSTIIDSTIIKVKVGDNQNLPSNRIFYDYSEYEDVTNDYA 518
QY 246 TFPNPQYKVEFNTPDDQITTPYIVVNGHIDPNSKGD-----LALRSTLYGYSNII 298
Db 519 QLGNNNDVAINFG---NIDSPYIIKVISKYDPN-KDYYTTIIQQTVMQTTINEYTG-- 571
QY 299 WRSMWDNEVAFNNGSGSGDGIDKPVVPEQ 328
Db 572 FRTASYDNTIAFSTSSGQGG-DLP--PEK 598

RESULT 10
Q8CQ72 PRELIMINARY; PRT; 1056 AA.
ID Q8CQ72;
AC Q8CQ72;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding
DE protein.

```
GN SE0331.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
  Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016745; AAC03928.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF05738; Cna_B_2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Complete proteome.
SQ SEQUENCE 1056 AA; 115728 MW; 015869A955CA2723 CRC64;

Query Match 20.2%; Score 349; DB 16; Length 1056;
Best Local Similarity 30.3%; Pred. No. 2.4e-11;
Matches 100; Conservative 61; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLTNVTGVI-DSGTIVYPHQAGYVKLNYSFVNSAVKGDTFKITYPKELNLNGVTS 71
Db 287 VTDQ--SITEGYDDESEGYKAHDAENLIYDVTFEYDDKVKSGDTMTVDIDKNTVPSDLTD 344
QY 72 TAKVPPIMAGD-QVLANGVIDS-DGNVIYTFDYVNTKDVKATLTMPAYIDPENVKKTG 129
Db 345 SFTIPKIKDNGSEIIATGYDNKNKQITFTFDYVDKYNIKAKHLKLTSTYIDSKVPMNN 404
QY 130 ---NVTLATIGSTANKTVLVDEYKGYKFNLSIKGTIDQIDKTNNTYRQTIYVNPSSG 186
Db 405 TKLDVEYKTLSS--VNKTTVEYQRPENENRTANLQSMFTNIDTKNHTVEQTIYINPL-- 460
QY 187 NVIAPVLTLGNLKPNTDSNALIDQNTSIXKYKYDNAADLSESYFV-NPENFEDVTSVNI 245
Db 461 RYSAKETNVNISGNDEGSTIIDSTIIKVKYGVGNQNLPSNRIRYDSEYEDVTNDYYA 520
QY 246 TFPNPNOYKVEFNTPPDQITTPYIVVNGHIDPNSKGD-----LALRSTLYGYSNII 298
Db 521 QLGNNNDVNINFG---NIDSPYIIKVISKYDPN-KDYTTTIQQTVMQTINEYTGE-- 573

QY 299 WRMSWDNEVAFNNGSGSGDIDKPVPEQ 328
Db 574 FRTASYDNTIAFSTSSGQGG-DLP--PEK 600

RESULT 11
ID 070022 PRELIMINARY; PRT; 1092 AA.
AC 070022;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Fibrinogen-binding protein precursor.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB;
RX MEDLINE=98261511; PubMed=9596732;
RA Nilsson M., Frykberg L., Flock J.I., Pei L., Lindberg M., Guss B.;
RT "A Fibrinogen-binding protein of Staphylococcus epidermidis.";
RL Infect. Immun. 66:2666-2673(1998).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
  AN AMIDE BOND (BY SIMILARITY).
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DR EMBL; Y17116; CAA76638.1; -.
DR PIR; T30214; T30214.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF05738; Cna_B_2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Cell wall; peptidoglycan-anchor; Signal.
FT SIGNAL 51
FT CHAIN 1
FT SEQUENCE 1092 AA; 119292 MW; 6542BC39AAD8B984 CRC64;

Query Match 20.2%; Score 349; DB 2; Length 1092;
Best Local Similarity 30.3%; Pred. No. 2.5e-11;
Matches 100; Conservative 61; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLTNVTGVI-DSGTIVYPHQAGYVKLNYSFVNSAVKGDTFKITYPKELNLNGVTS 71
Db 287 VTDQ--SITEGYDDESEGYKAHDAENLIYDVTFEYDDKVKSGDTMTVDIDKNTVPSDLTD 344
QY 72 TAKVPPIMAGD-QVLANGVIDS-DGNVIYTFDYVNTKDVKATLTMPAYIDPENVKKTG 129
Db 345 SFTIPKIKDNGSEIIATGYDNKNKQITFTFDYVDKYNIKAKHLKLTSTYIDSKVPMNN 404
QY 130 ---NVTLATIGSTANKTVLVDEYKGYKFNLSIKGTIDQIDKTNNTYRQTIYVNPSSG 186
Db 405 TKLDVEYKTLSS--VNKTTVEYQRPENENRTANLQSMFTNIDTKNHTVEQTIYINPL-- 460
QY 187 NVIAPVLTLGNLKPNTDSNALIDQNTSIXKYKYDNAADLSESYFV-NPENFEDVTSVNI 245
Db 461 RYSAKETNVNISGNDEGSTIIDSTIIKVKYGVGNQNLPSNRIRYDSEYEDVTNDYYA 520
QY 246 TFPNPNOYKVEFNTPPDQITTPYIVVNGHIDPNSKGD-----LALRSTLYGYSNII 298
Db 521 QLGNNNDVNINFG---NIDSPYIIKVISKYDPN-KDYTTTIQQTVMQTINEYTGE-- 573

QY 299 WRMSWDNEVAFNNGSGSGDIDKPVPEQ 328
Db 574 FRTASYDNTIAFSTSSGQGG-DLP--PEK 600

RESULT 12
ID 08NX5 PRELIMINARY; PRT; 1141 AA.
AC 08NX5;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Ser-Asp rich fibrinogen-binding bone sialoprotein-binding
  protein.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
  Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
  Yamamoto K., Hiramatsu K.;
RA "Genome and virulence determinants of high virulence community-
  acquired MRSA.";
RT Lancet 359:1819-1827(2002).
RL EMBL; AF004823; BAB94383.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpos_Ysirk.
```

DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF05738; Cna_B; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Complete proteome.
SQ SEQUENCE 1141 AA; 123997 MW; 372E5860850A332C CRC64;

Query Match 18.9%; Score 326.5; DB 16; Length 1141;
Best Local Similarity 31.5%; Pred. No. 4.7e-10;
Matches 112; Conservative 52; Mismatches 137; Indels 55; Gaps 18;

QY 2 VAADAPAGTDITNQLTNVT-----VGIDSGTTVYPHQAGYKLNFGFSVPNSAVKGDITF 56
DB 264 VAQPAVASNNV-NDLIKVTQKQIKVGDKNVAAAHDKDIEYDTEFTIDNKKKGDITM 322
QY 57 KI-----TVPKEINLNGVTSTAKVPFIMAGD---QVLANGVID-SDGNVIYFTDYVNTK 107
DB 323 TINYDKNVIPSDL-----TDKNDFIDITDPSGEVIAKGFDPKATKQITTYTFTDYVDKY 375
QY 108 DDVKATLTMPAYIDPENV--KKTGNVTIATGIGSTTANKTVLVDYEKYGKFNLSIKGTI 165
DB 376 EDIKSRLLTYSYIDKKTVPNETSLNLTFAAGKETSON--VTVDYQDPMVHGDSNIQSIF 433
QY 166 DQIDKTNNTYRQTIYVNP---SGDNVIAPVL-----TGNLKPNTDSNALIDQNTSIKY 216
DB 434 TKLDEDKQITEQGIYVNPFLKKSATNTKVDLAGSQVDYDGNIKLGNGS-TIID-QNTEIKY 491
QY 217 YKVDNADLSESYFV-NPENFEDVTNSVNTFEPNQKVEFNTPD-DQITPYIVVNG 274
DB 492 YKVNSDQQLPQSNRIYDFSQYEDVTSQ----FDNKKSFNNVATILDFGDISAYTIKIVS 547
QY 275 HIDPNSKGDL-----ALRST-LYGYNSNIIWRSMWDNEVAFNNGSGSGDGIDKP 323
DB 548 KYTPTSDGELDIAGCTSMRTTDKYG-----YNYAGYSNFIYVTSNDSGGGDTVKP 598

RESULT 13

ID Q99RD2 PRELIMINARY; PRT; 1038 AA.
AC Q99RD2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fnb protein (Fibronectin-binding protein homolog).
GN FNB OR SAV2503 OR SA2291.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoeyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003365; BAB58665.1; -
DR EMBL; AP003137; BAB43594.1; -
DR PIR; H90053; H90053.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Fn_bind.

DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind; 1.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KM Complete proteome.
SQ SEQUENCE 1038 AA; 113618 MW; 666BF6BF2BFBE12 CRC64;

Query Match 18.7%; Score 324.5; DB 16; Length 1038;
Best Local Similarity 26.9%; Pred. No. 5.4e-10;
Matches 91; Conservative 68; Mismatches 154; Indels 25; Gaps 11;

QY 10 GTDITNQLTNVTGIDS--GTTVYPHQAGYKLNFGFSVPNSAVKGDTEKITVPKELNLN 67
DB 189 GTDVTSKVTESGSEIEAPQGNKVEPHAGQVVLKYLKFKADGLKRGDYDFTLNNVNTY 248
QY 68 GVTSTAKVPPIMAGDQVLANGVIDSDGNVYFTDYVNTKDVKATLTMPAYIDPENVKX 127
DB 249 GVTSTARKVPEIKNGSVMATGEILGNRIYFTTNEIEHKVEYTNLEINLFIIDPKTVQS 308
QY 128 TGNVTIATGISTTANKTVLVDYEKYGKFNLSIKGTIDQIDKTNNTYRQTIYVNPSCDN 187
DB 309 NGEQKITSKLNGEETKTIPIVYNPGVNSYTNVNGSIETFNKSNKFTHIAYIKPMNGN 368
QY 188 VIAPV-LTGNLKPNTDSNALIDQNTSIKYK-VDNAADLSESYFVNPEN---FEDVTNS 242
DB 369 QSNVTSVTGTL---TEGSNLAGGQPT-VKYYEYLGKDELPGSVYANTSDTNKFKDVTKE 424
QY 243 VN--ITFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYG-----YNS 295
DB 425 MNGKLSVQDNGSYSLNL---DKLDKTYVIHYTGEYLGQS-DQVNFRTellyGPERAYKS 479
QY 296 NIWRS--MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 331
DB 480 YVYVGGRLLTWDNGLVLYSNKADGNGKNGQIIONDFE 517

RESULT 14

ID O86489 PRELIMINARY; PRT; 1166 AA.
AC O86489;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sdr E protein.
GN SDR E.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Newman;
RX MEDLINE=99098700; PubMed=9884231;
RA Josefsson E., McCrea K., Ni Eidhin D., O'Connell D., Cox J., Hook M.,
RA Foster T.J.;
RT "Three new members of the serine-aspartate repeat protein multigene
RT family of Staphylococcus aureus."
RL Microbiology 144:3387-3395(1998).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
DR EMBL; AJ005647; CA006652.1; -
DR PIR; T28680; T28680.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpos_YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF05738; Cna_B; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIRK_signal; 1.

DR TIGRFAMS; TIGR01167; LPXTG anchor; 1.
DR TIGRFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SEQUENCE 1166 AA; 126548 MW; 750A7B0135287D4A CRC64;

Query Match 18.7%; Score 323.5; DB 2; Length 1166;
Best Local Similarity 31.2%; Pred. No. 7.1e-10;
Matches 111; Conservative 53; Mismatches 137; Indels 55; Gaps 18;

QY 2 VAADAPAGTDTNQLTNTV-----VGIDSGTIVYPHQAGYVKLNYSFVNSAVKGDTE 56
DB VAQPAVASNNV-NDLIKVTQTIKVGDKDNVAAAHDKDIEYDTEFTIDNKVKKGDIM 327
QY KI-----TVPKELNLNGVSTAKVPPIAGD---QVLANGVID-SDGNVIYTFDYNTK 107
DB TINYDKNVIPSDL-----TDKNDPIDITDPGSEVIAGTFDKATKQITTYFTDYVDKY 380
QY 108 DDVKATLTMPAYIDPENY--KKTGNVTLATGISTTANKTVLVLDYEKGKFNLSIKGTI 165
DB EDIKSRLLTLYSIDKTVPNETSINLTFATAGKETSON--VTVDYQDPWVHGDSNIQSI 438
QY 166 DQIDKTNNTYRQTIYVNP---SGDNVIAPVL-----TGNLKPNLSDNALIDQNTSIKV 216
DB TKLDEDKQIEQIYVNPPLKKSATNTKVDIAGSQVDYGNIKLGNGS-TIID-QNTEIKV 496
QY 217 YKVDNAADLSESYFV-NPENEDVTNSVNITFPENQYKVEFNTPD-DQITTPYIVVNG 274
DB YKVNSDQQLPQSNRIYDFSQYEDVTSQ---FDNKKSFNNVATLDFGDINSAYIIKIVS 552
QY 275 HDPNSKGDL-----ALRST-LYGYNSNIWRSMWDNEVAFNNGSGSGDIDKP 323
DB KYTPTSDEGLDIAQGTSMRTIDKGY-----YNYAGYSNFIVTSNDTGGGDTYKP 603

RESULT 15

Q8KR22 PRELIMINARY; PRT; 566 AA.
AC Q8KR22;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Serine-aspartate repeat protein (Fragment).
OS Staphylococcus caprae.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=29380;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=89320;
RA Aubert S., Allignet J., Dyke K.G.H., Ryden C., El Solh N.;
RT "Staphylococcus caprae gene encoding a serine-aspartate repeat
protein."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY048594; AAL08114.1; -.
FT NON TER 1
SQ SEQUENCE 566 AA; 62896 MW; 0506759E2AFD3284 CRC64;

Query Match 18.6%; Score 323; DB 2; Length 566;
Best Local Similarity 29.7%; Pred. No. 3.1e-10;
Matches 89; Conservative 58; Mismatches 121; Indels 32; Gaps 12;

QY 4 ADAPAGTDTNQLTNTVGTGIDSGTIVYPHQAGYVKLNYSFVNSAVKGDTEFKITVPE 63
DB ANSEQGGSNVNDKI-NVDSFNVSKSDPNSGYSDDLNASFSVNGKIKEGDYFTVKYPR 323
QY 64 LNLNG-----VTSTAKVPPIM-AGDQVLANGVIDSDGNV-YTFDYVNTKDDVKATLT 115
DB VTVNGDVNTEKLNQMKVKPLTNANGDVVANGIYDVNSKTVKTYFTTNFVNDRNNIKGNFK 383
QY 116 MPAYIDPENYKKTGNVTLATGISTTANKTVLVLDYEK---YGKFNLSIKGTIDQID-- 169
DB LPIFTDRKNTPHSGNYSSTFNADKNTYETLINISYDSPYQGIKDAYGPNISSFITDIDLH 443

QY 170 KTNNTYRQTIYVNS-----GDNVIAPVLGNLKPNTDSNALIDQNTSIKVKVDNAAD 224
DB SGSEDFKQKIYVMENTLNSNV---RIQGYQTDQSKSSTIID-KNTKFKIYQKDAQ 499
QY 225 LSESYF--VNPENEDVTNSVN--ITFPENQYKVEFNTPDQITTPYIVVNGHIDPNS 280
DB LSESYNDTNSNLVDVTNNFNGWITVNSDNSVNIQFG---HIDGAYIIIEVGKYDSKS 555

Search completed: March 26, 2004, 05:07:43
Job time : 101.661 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:51:26 ; Search time 19.9539 Seconds
(without alignments)
863.752 Million cell updates/sec

Title: US-10-056-052A-4
Perfect score: 1732
Sequence: 1 MVADAPAPAGTDITNQLTNV.....NGSGSGDIDKPVVEQPD 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331	19.1	1018	1 FNBA_STA	P14738 staphylococ
2	129	7.4	762	1 SLAP_ACE	P22258 acetogenium
3	128	7.4	2021	1 OMPA_RIC	O52657 rickettsia
4	127	7.3	642	1 FLID_CAM	Q9phw6 campylobact
5	121.5	7.0	2249	1 OMPA_RIC	P15921 rickettsia
6	120.5	7.0	612	1 DNAK_OCE	Q8epw4 oceanobacil
7	119.5	6.9	544	1 GP10_DIC	Q06885 dictyosteli
8	117	6.8	856	1 ALE7_AZO	Q9zfg9 azotobacter
9	115.5	6.7	928	1 PM11_CHL	O86164 chlamydia p
10	114.5	6.6	1643	1 OMPB_RIC	Q53020 r outer mem
11	114	6.6	738	1 Y013_BPL	P42548 bacterioph
12	113.5	6.6	1228	1 SLAP_BAC	P35825 bacillus st
13	113.5	6.6	1250	1 YFAL_ECO	P45508 escherichia
14	113.5	6.6	1902	1 P1P_LAC	P16271 lactococcus
15	113.5	6.6	1902	1 P2P_LAC	Q02470 lactobacill
16	113.5	6.6	1902	1 P3P_LAC	P15292 lactococcus
17	113	6.5	1286	1 AIDA_ECO	Q03155 escherichia
18	113	6.5	1394	1 HAP_HAE	P45387 haemophilus
19	112	6.5	1902	1 P2P_LAC	P15293 lactococcus
20	111	6.4	995	1 Y1Q9_YEA	P40442 saccharomyc
21	110.5	6.4	1176	1 SLAP_BAC	P38537 bacillus sp
22	110.5	6.4	1645	1 OMPB_RIC	P96989 r outer mem
23	110	6.4	1183	1 CNA_STA	Q53654 staphylococ
24	109.5	6.3	760	1 SIX4_HUM	Q9uiu6 homo sapien
25	108.5	6.3	2003	1 YDBA_ECO	P33666 escherichia
26	108	6.2	827	1 CSG_HAL	P25062 halobacteri
27	108	6.2	2358	1 YEBT_ECO	P76347 escherichia
28	107.5	6.2	504	1 Y795_MET	Q58205 methanococc
29	107.5	6.2	1409	1 HAP1_HAE	P44596 haemophilus
30	107.5	6.2	1655	1 OMPB_RIC	Q9kka3 r outer mem
31	107	6.2	583	1 API_KLU	P56095 kluyveromyc
32	107	6.2	1698	1 41_DROM	Q9v8r9 drosophila
33	106.5	6.1	1181	1 ITA2_HUM	P17301 homo sapien

34	106	6.1	1562	1 SPAP_STR	P23504 streptococc
35	105.5	6.1	402	1 FLGE_SAL	P16322 salmonella
36	105.5	6.1	444	1 SLAP_LAC	P35829 lactobacill
37	105.5	6.1	544	1 PME3_LYC	Q96576 lycopersico
38	105.5	6.1	2452	1 RPB1_PLA	P14248 plasmodium
39	105	6.1	537	1 TEE6_STR	P18481 streptococc
40	105	6.1	655	1 YKDA_MYC	P45615 mycoplasma
41	105	6.1	906	1 Y010_CLO	Q97n28 clostridium
42	105	6.1	928	1 PMP9_CHL	Q92398 chlamydia p
43	105	6.1	1565	1 PAC_STR	P1657 streptococc
44	104.5	6.0	448	1 FIBP_ADE	Q83457 porcine ade
45	104.5	6.0	870	1 P100_HSV	Q00701 human herpe

ALIGNMENTS

RESULT 1
FNBA_STA
ID FNBA_STA STANDARD; PRT; 1018 AA.
AC P14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibronectin-binding protein precursor (FNBP).
GN FNBA.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucel G., Joensen K., Lindgren P.-E.,
RA Anantharamaiah G.M., Hoeoek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein
RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides."
RT Proc. Natl. Acad. Sci. U.S.A. 86:699-703 (1989).
CC -1- FUNCTION: THE ABILITY OF BACTERIA TO BIND FIBRONECTIN HAS BEEN
CC PROPOSED AS A VIRULENCE FACTOR ENABLING BACTERIA TO COLONIZE
CC WOUND TISSUES AND BLOOD CLOTS. BINDING OF PLASMA FIBRONECTIN TO
CC THE BACTERIAL SURFACE MIGHT BLOCK ADHESION RECEPTORS ON S.AUREUS,
CC THUS REPRESENTING AN IMPORTANT DEFENSE MECHANISM AGAINST TISSUE
CC INVASION.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J04151; AAA26632.1; -;
CC InterPro: IPR004237; Fn_bind.
CC InterPro: IPR005877; Gpos_Y5IRK.
CC InterPro: IPR001899; Gram_pos_anchor.
CC Pfam: PF02986; Fn_bind; 1.
CC Pfam: PF00746; Gram_pos_anchor; 1.
CC Pfam: PF04650; Y5IRK_signal; 1.
CC TIGRfams: TIGR01167; LPTXG_anchor; 1.
CC TIGRfams: TIGR01168; Y5IRK_signal; 1.
CC PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
CC Cell wall; Peptidoglycan-anchor; Repeat; Signal.
FT SIGNAL 1 36
FT CHAIN 37 985 FIBRONECTIN-BINDING PROTEIN.
FT PROPEP 986 1018 REMOVED BY SORTASE (POTENTIAL).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X APPROXIMATE TANDEM REPEATS,
FT

FT REPEAT 745 782 FIBRONECTIN-BINDING DOMAIN.
FT REPEAT 783 820 D-1.
FT REPEAT 821 859 D-2.
FT REPEAT 860 878 D-3.
FT DOMAIN 879 948 5 X TANDEM REPEATS, PRO-RICH (WR).
FT REPEAT 879 892 WR1.
FT REPEAT 893 906 WR2.
FT REPEAT 907 920 WR3.
FT REPEAT 921 934 WR4.
FT REPEAT 935 948 WR5.
FT SITE 982 986 LPXTG SORTING SIGNAL (POTENTIAL).
FT MOD RES 985 985 AMIDE-LINKED TO CELL WALL (POTENTIAL).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81F1F CRC64;

Query Match 19.1%; Score 331; DB 1; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7,1e-13;
Matches 82; Conservative 77; Mismatches 146; Indels 28; Gaps 11;

QY 10 GTDITNQLTNVTVGIDSG---TTVYPHQAGYVKLNYGFSVPNSAVKGDTFKITVPKELN 65
DB 194 GTDVTSKVT-VEIGSIEGHNNNTNKVEFHAGQAVLKYLKFEENGHOGDYFDFTLSNNVN 252
QY 66 LNGVTSTAKVPIMAGDQVLANGVIDSDGNVITYFTDYNTKDYKATLTMPAYIDPENY 125
DB 253 THGVSTARKVPEIKNGSVVMATGEVLEGGKIRYFTNDIEDKVDVTALEINLFIDPKTV 312
QY 126 KKTGNVTLATGIGSTTANKTVLVYD-EKYGKFNLSIKGTIDQIDKTNNTYRQTIYVNP 184
DB 313 QTNNGQITITSTINEEQTSKELDVKKDIGNY-ANLNGSIEFTFNKANNRFSHVAFIKPN 371
QY 185 GDNVIAPVLGTNLKPNITSDNALIDQNTSIRYK-VDNAADLSESYFN--PENFEDVT 240
DB 372 NGKTTSVTVTGLMKGSNONG---NQPKVRIFEYLGNNEDIKSVYANTTDTSKFKEVT 427
QY 241 NSV--NITFPNPQYKVFENTPDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNII 298
DB 428 SNMSGNLNLQNNGSYSINI---ENLDKTYVHYDGEY-LNGTDEVDFRTQMGHPEQLY 482
QY 299 -----WRSMWDNEVAFNNGSGSGDIDKPVY 325
DB 483 KYYYDRGYTLTWNGVLVYSNKANGNEKNGPIT 515

RESULT 2
SLAP_ACEKI STANDARD; PRT; 762 AA.
ID SLAP_ACEKI
AC P22258;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cell surface protein precursor (S-layer protein).
OS Acetogenium kivui.
OC Bacteria; Firmicutes; Clostridia; Thermoaerobacteriales;
OC Thermoaerobacteriaceae; Thermoaerobacter.
OX NCBI_TaxID=2325;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=DSM 2030;
RX MEDLINE=90036724; PubMed=2681162;
RA Peters J., Peters M., Lottspeich F., Baumeister W.,
RT "S-layer protein gene of Acetogenium kivui: cloning and expression in
RT Escherichia coli and determination of the nucleotide sequence.",
RL J. Bacteriol. 171:6307-6315(1989).
RN [2]
RP PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.
RC STRAIN=DSM 2030;
RX MEDLINE=92281680; PubMed=1596358;
RA Peters J., Rudolf S., Oschkinat H., Mengede R., Sumper M.,
RA Kellermann J., Lottspeich F., Baumeister W.,
RT "Evidence for tyrosine-linked glycosaminoglycan in a bacterial
RT surface protein.",
RL Biol. Chem. Hoppe-Seyler 373:171-176(1992).

RN [3]
RP DOMAINS.
RX MEDLINE=94156823; PubMed=8113161;
RA Lupas A., Engelhardt H., Peters J., Santarius U., Volker S.,
RA Baumeister W.,
RT "Domain structure of the Acetogenium kivui surface layer revealed by
RT electron crystallography and sequence analysis.",
RL J. Bacteriol. 176:1224-1233(1994).
CC -1- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
CC of proteins which coat the surface of bacteria.
CC -1- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
CC layer with hexagonal symmetry.
CC -1- PTM: THE CARBOHYDRATE CONTENT OF THIS PROTEIN IS ABOUT 8% WHICH
CC CORRESPOND TO ABOUT 40 TO 50 SUGAR MOLECULES PER MONOMER. O-LINKED
CC GLYCANS CONSIST OF GLC, GALNAC AND GLCNAC.
CC -1- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
CC -----
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CC -----
DR EMBL, M31069; AAA21930.1; -.
DR PIR; A34355; A34355.
DR InterPro; IPR001119; SLH.
DR Pfam; PF00395; SLH; 2.
DR PROSITE; PS01072; SLH_DOMAIN; 2.
KW Signal; Glycoprotein; Repeat; Cell wall; S-layer.
FT SIGNAL 1 26
FT CHAIN 27 762 CELL SURFACE PROTEIN.
FT DOMAIN 30 94 SLH 1.
FT DOMAIN 95 145 SLH 2.
FT DOMAIN 146 204 SLH 3.
FT DOMAIN 473 479 SER/THR-RICH.
FT DOMAIN 625 630 SER/THR-RICH.
FT CARBOHYD 297 297 O-LINKED (GLC. . .).
FT CARBOHYD 516 516 O-LINKED (GLC. . .).
FT CARBOHYD 520 520 O-LINKED (GLC. . .).
FT CARBOHYD 632 632 O-LINKED (GLC. . .).
SQ SEQUENCE 762 AA; 82785 MW; 34EC9C784DECA67E CRC64;

Query Match 7.4%; Score 129; DB 1; Length 762;
Best Local Similarity 21.6%; Pred. No. 1.1;
Matches 79; Conservative 54; Mismatches 113; Indels 120; Gaps 19;

QY 15 NQLTNVTVGIDS-GTYVYPHQAGYVKLNYGFSVPNSAVKGDTFKITVPKELN---LNG- 68
DB 280 NDVVSFTGQDSVGTIVY-----KNDDNKTAIKVDNAYVLYNGY 319
QY 69 VTSTAKVP-----PIMAGDQVLANGVIDSDG---NVIYFTDYVN--TKDVKATLTM 116
DB 320 LTKVSKVTVKEGAETIINNYYLIVNGSYDNSTIYNDVQSGDKYLNKRDSEYELKGTIVT 379
QY 117 PAYIDPENVKKTGNVTLATGIGSTTANKTVLVYDYEKYGKFNLS-----IK 162
DB 380 -----TGAVSKVTDI--KAN-----DYIYKGQYDVNGVNGVTVYVRNQVT 420
QY 163 GTIDQIDKTNNTYRQTIYVNPSCDNLVAPVLGTN---LKPNITSDNALIDQNTSIRYK 218
DB 421 GTVTEKSVSGSTYKASI-----DNVSYTADNNVYVNGLEPGKVTVILANKNVIVGI-- 472
QY 219 VDNAADLSESYFVNPNFEDVTVSNITFPNPQYKVFENTPD-----DOI 264
DB 473 -----SSTTTTAVNVAIFEKSDPFTAWFA-----KVKLILPDAEKVFDAYVSDVYDKV 523
QY 265 TTPYIVVNGHIDPNSK-----GDALRSTLYGNSNIIWRSMS-----WNEVAFNNG 313
DB 524 NLAEGTIVTVVDANGKLANDIQRANDQPFSSASAYADAKVLTEGSTTYITITNTVLLNNT 583
QY 314 SGSGDG 319

Db 810 LRVGGVYKSNNTINLTDNASAVTFINPVVVTGAIDNTGNANNGI VFTGDSVTGNIGNT 869

QY 187 NVIAPVLTGNLKPNTDSNALIDQNTS1KVKYKVDNADLSESYFVNPFEDVINSVNT 246

Db 870 NALATISVGAKA-TLGGAIITKATTKL-----TDNASAVT---FTNP---VVVTGALDNT 918

QY 247 FPNPNQYKVEFNTPPDDQIT-----TPYIVVN-----GHIDPNSKGDALRSTL 290

Db 919 -GNANNGI VTF-TGDSVTGNIGNTNALATVNVGAGVTLQAGGSLDANNI-DFGARSTL 974

RESULT 4

ID FLID CAMJE STANDARD; PRT; 642 AA.

AC Q9PHW6; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Flagellar hook-associated protein 2 (HAP2) (Filament cap protein)

DE (Flagellar cap protein).

GN FLID OR CJ0548.

OS Campylobacter jejuni.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

OC Campylobacteraceae; Campylobacter.

OX NCBI_TaxID=197;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NCTC 11168;

RX MEDLINE=20150912; PubMed=10688204;

RA Parkhill J., Wren B.W., Mungall K., Kelsey J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S., Jagsels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.;

RA "The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";

RT Nature 403:665-668(2000).

CC -1- FUNCTION: REQUIRED FOR THE MORPHOGENESIS AND FOR THE ELONGATION OF THE FLAGELLAR FILAMENT BY FACILITATING POLYMERIZATION OF THE FLAGELLIN MONOMERS AT THE TIP OF GROWING FILAMENT. FORMS A CAPPING STRUCTURE, WHICH PREVENTS FLAGELLIN SUBUNITS (TRANSPORTED THROUGH THE CENTRAL CHANNEL OF THE FLAGELLUM) FROM LEAKING OUT WITHOUT POLYMERIZATION AT THE DISTAL END (BY SIMILARITY).

CC -1- SUBUNIT: Homopentamer (By similarity).

CC -1- SUBCELLULAR LOCATION: Flagellar.

CC -1- SIMILARITY: Belongs to the flid family.

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DR EMBL; AL139075; CAB75184.1; -.

DR PIR; D81401; D81401.

DR InterPro; IPR003481; FLID.

DR Pfam; PF02465; FLID; 1.

KW Flagellum; Coiled coil; Complete proteome.

FT DOMAIN 614 641 COILED COIL (POTENTIAL).

SQ SEQUENCE 642 AA; 69775 MW; 40FF20D41688EFA3 CRC64;

Query Match 7.3%; Score 127; DB 1; Length 642;

Best Local Similarity 20.9%; Pred. No. 1.1; Indels 142; Gaps 19;

Matches 86; Conservative 48; Mismatches 136;

QY 21 TVGIDSGTIVYPHQAGYVKLNYG---FSVPNSAVKGDTFKITV-PKELNLNGVTSTAKV 75

Db 146 TVTVDKNTT-YRDLADKINASGEIIVAKIVNTGEGKTPYRLTLTSKETGEDSAIS---- 200

QY 76 PRIMAGDQVLANGVIDSDGNVITYFTDYVNTKDVAKATLMPAYIDPENVKK----- 127

Db 201 --FYAGKRD-SNGKYQKDINAKEIF-----DDLGMGLDVSASIDPDKDKGYGIKDAS 250

QY 128 -----TGNVTLATGIGST-TANKVVLVDYEKKGFYNLSIKGTID 166

Db 251 LHIQTAQNAEFTLIDGKIMFRSSNTVTDLGVMTLTLNKGTGEINFDVQDQDFEGVT-KAMQD 309

QY 167 QIDKTN---NTYQTIY-----VNPSCDNVIAPVLTGNLKPNTDSNALI 207

Db 310 LVDAYNDLVTNMAATDYNSETGTGTGTLQGISVNSIRSSILADLPDSQVVDGTTEEDANG 369

QY 208 DQQNTSIKV-----YKVDNADLSESYFVNPFEDVT----- 240

Db 370 NKVNTKWLMSQDFGLSLNDAGTSLSPSSKFEQKVKEDPDSITSFFSNITKYEDINHTE 429

QY 241 -----NSVNITFPNPQYKVEFNTPPDDQIT-----TPYIVV 271

Db 430 VIKTGLSKYLNSNGNTNGLEF-KPGDFTIVFNNTQTYDLSKNSDGTNFKLTGKTEEEL 488

QY 272 VN--GHIDPNSKGDALRSTLYGYNSNIWRMSWDNEVAFN--NGSGSGD 318

Db 489 QNLANH1--NSKGIEGLKVKVESYNQN-----NVTGFRNFSGDSSD 529

RESULT 5

ID OMPA_RICRI STANDARD; PRT; 2249 AA.

AC P15921; 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).

GN OMPA.

OS Rickettsia rickettsii.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBI_TaxID=783;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=R;

RX MEDLINE=90354033; PubMed=2117568;

RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;

RT "A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";

RT Infect. Immun. 58:2760-2769(1990).

CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.

CC -1- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-layer with hexagonal symmetry.

CC -1- PTM: Glycosylated (Probable).

CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPA FAMILY.

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CC EMBL; M31227; AAA26380.1; -.

DR PIR; A41477; A41477.

DR InterPro; IPR006315; Autotransport.

DR InterPro; IPR005546; Autotransporter.

DR Pfam; PF03797; Autotransporter; 1.

DR TIGRFAMs; TIGR01414; autotrans_bar1; 3.

KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.

FT SIGNAL 1 28 POTENTIAL.

FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.

FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.

FT REPEAT 212 286 A (TYPE I).

FT REPEAT 287 358 B (TYPE II).

FT REPEAT 359 430 C (TYPE II).

FT REPEAT 431 505 D (TYPE I).

FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE II).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match 7.0%; Score 121.5; DB 1; Length 2249;
Best Local Similarity 22.3%; Pred. No. 12;
Matches 78; Conservative 38; Mismatches 144; Indels 89; Gaps 14;

QY 14 TNQLTNVTG-----IDSGTTVPHQAGYVKLNYGFSVPNSAVK---GDTFKIT 59
DB 878 TNSLATISVGAGTATLGGAVIKATTTKLTNAASVLTLTNANAVLTGAIDNTTGGDNVGV- 936
QY 60 VPKELNLNV-----TSTAKVPPIMAGDQVLANGVIDSDGNVIYFTDYNTKOD 109
DB 937 ---LNLGALSGVTGIDGNTNSLATISVGAGTATLGGAVIKA-----TTTKLTDAASA 986
QY 110 VKAT--LTMPAYIDPEN-----VKKTGNVTLATGIGSTTANKTV----- 146
DB 987 VKFTNPVVVTGAIDNTGNANNGIVTFTGNSFTVGNVNTNALATVAVGAGLLQVGGVVK 1046
QY 147 ----LVDEYKYGKFN-LSIKGTIDQDKTN----TYRQTIYVNSGDNVIAVPLIG 195
DB 1047 ANTINLTDNASAVTFNPPVVTGAIDNTGNANNGIVTFTGNSFTVGNVNTNALATVAVG 1106
QY 196 NLKPNTDSNALIDQNTSIKVKVDNAADLSSESYFVNP-----ENFEDVTNSVNITFP 248
DB 1107 -----AGLLQVGGVVKANTINLTNDNASAVTFNPPVVTGAIDNTGNANNGI-VTFT 1157
QY 249 NPNQKVEFNTPDDQITTPYIVVNGHIDPNSKGDALRSTLYGYSNI 297
DB 1158 GNSTVTGIDGNTNALAT---VNVGAGITLQAGGSLAANNIDFGARSTL 1202

RESULT 6
DNAK_OCEIH STANDARD; PRT; 612 AA.

ID_DNAK_OCEIH STANDARD; PRT; 612 AA.
AC Q8EPN4:
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Chaperone protein dnak (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70).
GN DNAK OR OB1968.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=2220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments."
RT Nucleic Acids Res. 30:3927-3935(2002).
RL -!- FUNCTION: Acts as a chaperone (By similarity).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
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CC -----
DR EMBL; AP004599; BAC13924.1; -.
DR HAMAP; MF_00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation;
KW Complete proteome.
FT MOD RES 173 173 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 612 AA; 66558 MW; 5097482DC007BB41.CRC64;

Query Match 7.0%; Score 120.5; DB 1; Length 612;
Best Local Similarity 20.7%; Pred. No. 2.6;
Matches 77; Conservative 54; Mismatches 106; Indels 135; Gaps 20;

QY 22 VGIDSGT-----VYPH-----QAGYVKLNYGFSVPNS- 49
DB 5 IGIDLGTTNSCVSVEGGEAVVIPNPEGNRTPSVVAFKNGERQVGEVAKRQAITNPNTI 64
QY 50 -AVK---GDTFKITV-----PKELN---LNGVSTAKVPPIMAGDQVLANGVIDSDGNV 96
DB 65 QSIKRMGTDYKVKIEKEKYPQEVSAIILQYIKSYAE----- 102
QY 97 IYFTDYNTKDDVAKTLTMPAYI---DPENVKKTGNV-----TLATGIG 138
DB 103 ----DYIGEKVE-KAVITVPAYFNDARQATYDAGKIAGLEVERIINEPTAALAYGID 156
QY 139 STTANKTVLVDEYKYGKFNLSIKGTIDQDKTNNTYRQTIYVNSGDNVIAVPLTGNLK 198
DB 157 KEDQDQITLV-YDLGGTFDVS-----LDIGDGTFE--VSTAGDN-----RLG 198
QY 199 PNTDSNALIDQNTSIKVKVDNAADLSSESYFVNPENFEDVTNSVNITPNNQKVEFN 258
DB 199 GDDFDQVIIDHM---VQEKKENAIDLSQDKAT-QRLKDAAEKAKKDLGVTQ----- 248
QY 259 TPDDQITTPYIVVNGHIDPNSKGDALRSTLY-----GYSNIIWRSMGWDNEVAFNG 313
DB 249 ---TQISLPFITA-----GDAGPLHLEMTMSRAKFDLSSDLVERTMQ-PTRKALSDA 297
QY 314 SGSGDGIDKPPV 325
DB 298 SLKSDIDKVL 309

RESULT 7
GP10_DICDI STANDARD; PRT; 544 AA.

ID_GP10_DICDI STANDARD; PRT; 544 AA.
AC Q06885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Glycoprotein gp100 precursor (P29F8).
GN GPPA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94124612; PubMed=8294503;
RA Barth A., Mueller-Taubenberger A., Taranto P., Gerisch G.;
RT "Replacement of the phospholipid-anchor in the contact site A glycoprotein of D. discoideum by a transmembrane region does not impede cell adhesion but reduces residence time on the cell surface."
RT J. Cell Biol. 124:205-215(1994).
RL -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DEVELOPMENTAL STAGE: Restricted to the aggregation stage of development in D.discoideum. No detectable activity in cell

DR SMART; SM00710; Pbh1; 9.
DR PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 6.
KW Alignate biosynthesis; isomerase; Calcium; Repeat; Multigene family.
FT REPEAT 97 125 Pbh1 1.
FT REPEAT 133 155 Pbh1 2.
FT REPEAT 157 179 Pbh1 3.
FT REPEAT 180 202 Pbh1 4.
FT REPEAT 204 226 Pbh1 5.
FT REPEAT 234 256 Pbh1 6.
FT REPEAT 257 279 Pbh1 7.
FT REPEAT 280 304 Pbh1 8.
FT REPEAT 320 342 Pbh1 9.
FT REPEAT 386 403 Hemolysin-type calcium-binding 1.
FT REPEAT 404 421 Hemolysin-type calcium-binding 2.
FT REPEAT 422 439 Hemolysin-type calcium-binding 3.
FT REPEAT 537 554 Hemolysin-type calcium-binding 4.
FT REPEAT 555 572 Hemolysin-type calcium-binding 5.
FT REPEAT 573 590 Hemolysin-type calcium-binding 6.
FT REPEAT 714 731 Hemolysin-type calcium-binding 7.
FT REPEAT 732 749 Hemolysin-type calcium-binding 8.
FT MUTAGEN 152 152 D->G: LOSS OF BOTH EPIMERASE AND LYASE
FUNCTIONS.
SQ SEQUENCE 856 AA; 90364 MW; 626DDCA4681E8807 CRC64;
Query Match 6.8%; Score 117; DB 1; Length 856;
Best Local Similarity 21.8%; Pred. No. 6.6;
Matches 82; Conservative 52; Mismatches 127; Indels 116; Gaps 20;
QY 8 AAGTDITNQLTNTVIGIDSGTIVYPHQAGYVKLNYSVPNSAVKGDFTKLTVPKELNLN 67
Db 344 ADGTDYTS-IGNNSV---SGT-----QRGIVQLS-GTNSTFSGRSGDAYQF-----ID 386
QY 68 GVTSTAKV--PIM-----AGDQVLANG-----VIDSDGNVYFTD--- 102
Db 387 GSTGNDLLTGTPADLIVGGSGNDTSLSGDAGNDVLEGGAGSDRLTGEGADIFRFTAVSD 446
QY 103 --YVNTKDDYKATLTMPAYIDPENVKKTGNVTLATIGSTTA-----NKTVLVDEYK- 152
Db 447 SYTRASSSVADQILDFDASNDRIDLTGLGFTGLGDYGTLLAVLANSDSRITLRSYEKD 506
QY 153 -YGRYVNLISIKGT-IDQIDKTNNTYRQTIYVNPSCD-----NVIAPVLTGNLKNTDS-- 203
Db 507 ADGRYFSLTLDGNFVGRLLDSNLVFRHKTIAEGEDSLTGNAEAELIDCG--SGNDSL 564
QY 204 -----NALIDQNTS---IKVYKVDNAADLSESYFVNPNEDVTNS 242
Db 565 GGLGNDVLRGAGDDILNGGLGRDQLSGEGADIFRFTSVAD---SYQNSGDNFSDLI-- 619
QY 243 VNITFENPNQYKVEFNTPPDDQTTPIYVNVGHIDPNKGDALRSTLYGYSNIIWRSM 302
Db 620 -----LDFDPGEDR-----IDLSGIGFSGGLGD--GHNGTILLMTS 652
QY 303 SWDNEVAFNNGSGSGDG 319
Db 653 SETNRTYLNKMFDTDADG 669
RESULT 9
Pml1_CHLPN STANDARD; PRT; 928 AA.
ID Pml1_CHLPN
AC 086164; Q9K299;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DE 10-OCT-2003 (Rel. 42, last annotation update)
DE Probable outer membrane protein pml1 precursor (Polymorphic membrane
protein 11) (Outer membrane protein 4).
GN Pml1 OR OMP4 OR CPN0449 OR CP0302 OR CPB0468.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029/VR-1310;

RX MEDLINE=99081766; PubMed=9864239;
RA Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;
RT "Identification of two novel genes encoding 97- to 99-kilodalton outer
RL membrane proteins of Chlamydia pneumoniae.";
RN Infect. Immun. 67:375-383(1999).
RP [2]
RC SEQUENCE FROM N.A.
RX STRAIN=VR1310;
RA MEDLINE=20007584; PubMed=10539856;
RT Christiansen G., Boesen T., Hjerno K., Dagaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk B., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
RL role in immunopathogenicity.";
RN Am. Heart J. 138:S491-S495(1999).
RP [3]
RC SEQUENCE FROM N.A.
RX STRAIN=CWL029;
RA MEDLINE=99206606; PubMed=10192388;
RT Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RN Nat. Genet. 21:385-389(1999).
RP [4]
RC SEQUENCE FROM N.A.
RX STRAIN=AR39;
RA MEDLINE=20150255; PubMed=10684935;
RT Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RT Eisen J., Fraser C.M.;
RL "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RN Nucleic Acids Res. 28:1397-1406(2000).
RP [5]
RC SEQUENCE FROM N.A.
RX STRAIN=J138;
RA MEDLINE=20330349; PubMed=10871362;
RT Shitai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RL from Japan and CWL029 from USA.";
RN Nucleic Acids Res. 28:2311-2314(2000).
RP [6]
RC SEQUENCE FROM N.A.
RX STRAIN=TW-183;
RA Geng M.M., Schumacher A., Muehlhofer I., Bensch K.W., Schaefer K.P.,
RT Schneider S., Pohl T., Essig A., Warte R., Melchers K.;
RL "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
other Chlamydia strains based on whole genome sequence analysis.";
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases
CC -I- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies
CC (potential)).
CC -I- SIMILARITY: Belongs to the PMP outer membrane protein family.
CC -----
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CC -----
DR EMBL; AJ001311; CA04672.1; -;
DR EMBL; AJ133034; CAB37072.1; -;
DR EMBL; AE001628; AAD18593.1; -;
DR EMBL; AE002192; AAF38159.1; ALT_INIT.
DR EMBL; AP002546; BAA98658.1; -;
DR EMBL; AE017158; AAP98399.1; -;
DR PIR; D72077; D72077.
DR PIR; H86546; H86546.
DR PHCI-2DPAGE; 086164; -;
DR TIGR; CP0302; -;

[illegible][illegible]

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QY      156 FYNLSIKGTIDQIDKTN--TYRQTIYWP-----SGDNVIAPVLTGN-----196
Db      514 Y-----KITVQAVDPSPGNIGTLTRTIIVWVDGIGPVFENGINTITASINENITVEQIKAGLA 568
QY      197 ----LKENTDSNALIDQCN-----TSIKVYK-----VDNAAD-----LSESYFVNPENFE 237
Db      569 AIDAIDGNVTTTSIIVDSDNLTGKANTVGVYEVERAIVDAAGNQTFFHTVTSIVASPPGFY 628
QY      238 DV-TNSVNVITEFPNP-----QYKVEFNTPD-DQITPYIYVWNGHIDENSKGDLALRSTLY 291
Db      629 IINSNSVRL-LPGANLTIEQILINTINASDAENISTNYTIVSVPGTYN-----LSFTLY 679
QY      292 GYNSNIIRSMMSWDNEVAFNNGSGSGDDGIDKPVVP 326
Db      680 GESHQVSVITVLGQNDST-----IPTPVIP 703

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RESULT 12
SLAP_BACST
ID SLAP_BACST STANDARD; PRT; 1228 AA.
AC P35825;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE S-layer protein precursor (Surface layer protein) .
GN SBSA.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=PV72;
RX MEDLINE=94320770; PubMed=8045409;
RA Kuen B., Sleytr U.B., Lubitz W.;
RT "Sequence analysis of the sbsA gene encoding the 130-kDa
RL surface-layer protein of Bacillus stearothermophilus strain PV72.";
Gene 145:115-120(1994).
CC -|- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
CC of proteins which coat the surface of bacteria.
CC -|- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
CC layer with hexagonal symmetry.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X71092; CAA50409.1; -.
DR EMBL; AX000218; CAB77069.1; -.
DR PIR; I40468; I40468.
KM Signal; Cell wall; S-layer.
FT SIGNAL. 1 30 POTENTIAL.
FT CHAIN 31 1228 S-LAYER PROTEIN.
SQ SEQUENCE 1228 AA; 131076 MW; 9F1383AD810C0B0F CRC64;

Query Match 6.6%; Score 113.5; DB 1; Length 1228;
Best Local Similarity 22.1%; Pred. No. 17;
Matches 90; Conservative 51; Mismatches 139; Indels 127; Gaps 24;

QY 12 DITNQLTNVTG-----IDSGTVPYPH-----QAGYVKLNGFSV---PNS 49
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 769 DAVTLLTNVDAGQKFTIQSEELKTSSGSLVGKQVTEKLTNNNGVVDAGTGTVSVAPE 828
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 50 AVKGDTEFKITVPKELNNGVSTAKVPPI-MAGDQVLANGVIDSDGNVI-----YFTTD 102
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 829 DANG---KYTA-AVVTLTGLDNNNDKDAKRLRVVDKSSITDGIADVAGNVIKEKDIILRYS 884
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 103 YVNT-----KDDVKATLTMP-----AYIDPENV---KKTGN 130
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 885 WRHTVASVKAADKDGQNASAAFPSTAIIDTTKSLVFNENETDLAEVKPENIVVKDAQGN 944

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QY 131 VTLATGI--GSTTANKTVLVDE--KYGKFYNLSIKGTIDQDKTNNTY--RQTIYVN 182
DB 945 AVAGTVTALDGST--NKFVFTPSQELKAGTVSVTIDGVRDKVGNNTISKYITSEKTVSAN 1002
QY 183 PSGDNVIAPVLTGNLKPNTDSNALIDQ-----NTSIKYKVVDNADLSESYFVNPENF 236
DB 1003 PT---LSSISIADGAVNVDRSKTITIEFSDSVPNPTITLKKADG----- 1043
QY 237 EDVTVNSVNITFPNPNQ---YKVEFN---TPDDQITTPYIVVNGHI---DPNSK---- 281
DB 1044 ---TSFTNYTLVNVNENNKTYKIVFHKGVTLDE--FQYELAVSKDFQTGTIDISKVTFI 1098
QY 282 -GDLA---LRSTLYGYNSNIWRSMSWDNEVAFNNGSGSGDGDIDKPV 324
DB 1099 TGSVAVDEVKPALVGVGS---WNGTSYTGQDAATRLRSVADFEVAPV 1142

RESULT 13

YFAL_ECOLI STANDARD; PRT; 1250 AA.
AC P45508; P39441; P45506; P45507; P76468; P77487;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yfal precursor.
GN YFAL OR B2233.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA Oshima T., Oyama S., Saito N., Sempel G., Satch Y., Sivasundaram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT - K12 genome corresponding to 50,0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
RN [3]
RP PRELIMINARY SEQUENCE OF 1-938 FROM N.A.
RX MEDLINE=84272624; PubMed=6087316;
RA Carlson J., Fuchs J.A., Messing J.;
RT "Primary structure of the Escherichia coli ribonucleoside diphosphate
RT reductase operon.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4294-4297(1984).
RN [4]
RP SEQUENCE OF 925-1198 FROM N.A.
RC STRAIN=K12 / EMG2;
RA Estep P., O'Keefe T., Robison K., Church G.M.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1180-1250 FROM N.A.
RC STRAIN=OV6;
RX MEDLINE=88201664; PubMed=2834621;
RA Hussain K., Elliott E.J., Salmond G.P.C.;
RT "The pard- mutant of Escherichia coli also carries a gyrAam mutation.

RT The complete sequence of gyrA.";
RL Mol. Microbiol. 1:259-273(1987).
RN [6]
RP IDENTIFICATION.
RX MEDLINE=96032851; PubMed=7567469;
RA Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
RA Danchin A.;
RT "Detection of new genes in a bacterial genome using Markov models for
RT three gene classes.";
RL Nucleic Acids Res. 23:3554-3562(1995).
CC -!- SIMILARITY: TO E.COLI YDEK.
CC -!- CAUTION: Ref.3 sequence differs extensively from that shown by
CC many frameshifts.
CC -----
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CC -----

DR EMBL; AE000313; AAC75293.1; -.
DR EMBL; D90855; BAA16052.1; ALT_INIT.
DR EMBL; D90854; BAA16050.1; ALT_INIT.
DR EMBL; K02672; -; NOT_ANNOTATED_CDS.
DR EMBL; U30459; AAA74094.1; -.
DR EMBL; Y00544; -; NOT_ANNOTATED_CDS.
DR PIR; G64993; G64993.
DR EcoGene; EG12850; yfal.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia_PMP.
DR InterPro; IPR004899; Pertactin.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF02415; Chlamydia_PMP; 1.
DR Pfam; PF03212; Pertactin; 1.
DR TIGRFAMS; TIGR01414; autotrans_bar1; 2.
DR TIGRFAMS; TIGR01376; POMP_repeat; 4.
DR Hypothetical protein; Repeat; Signal; Complete proteome.
KW SIGNAL
FT 1 23
FT CHAIN 24 1250
FT DOMAIN 919 948
FT CONFLICT 28 30
FT CONFLICT 40 40
FT CONFLICT 65 66
FT CONFLICT 431 431
FT CONFLICT 433 434
FT CONFLICT 478 478
FT CONFLICT 773 773
FT CONFLICT 853 853
FT CONFLICT 923 924
FT CONFLICT 948 994
SQ SEQUENCE 1250 AA; 131152 MW; 17F98C05E29FC95 CRC64;
LRYVIGG -> LITSRC (IN REF. 4).
PAYQPVLNKAVGGLNNLRANAQAEMERRDHAGDGQTLN

Query Match 6.6%; Score 113.5; DB 1; Length 1250;
Best Local Similarity 21.9%; Pred. No. 18;
Matches 90; Conservative 45; Mismatches 137; Indels 139; Gaps 19;
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DB 618 SDAAGHGRDIEMRADGEVAVDGTQGMALMADSSGQHODEGSTLTKTGAGTLELTASG 677
QY 41 --NYGFSVPNSAVKGDTFKITVPEKELN---NGVTSTAKVPEPIMAGDQVLANGVTD-SDG 94
DB 678 TTQSAVRVEEGTLKGDVADI-LPYASSLWVGDGATFVTGADQDIDQSIDAISSGTTIDSDG 736
QY 95 NVI-YTFTD-----YVNTKDDVKATLTMPAYIDPE-----NVKKTGNVT 132
DB 737 TVLRRLTGQDTSVALNASLFGNGDGLVNATDGVTLTGELNLTNLETDSLTYLSNVTVNGNL 796
QY 133 LATGI-----GSTTANKTVLVDEYKYGKFNLSIKGTIDQDKTNNTYRQ 177

Db 797 NTSGAVSLQNGVAGDTLTVNGDYTGCGTLLLDSELNGD-----DSVSDQLVNMNGTAGN 850
Qy 178 TIYVNSGDNVIAPLVTGNLKPNTDSNALIDQNTSISKYKVDNAD-----LS 226
Db 851 T-----TVVNSITGIGEP-----STGIKV--VDFADPTQFQNNAGSLSA 890
Qy 227 ESYFVN-----PENFEDVTNSVNT-----FPNPNOYKVEFNTPPDDQITPY 268
Db 891 GSGYVNMGAYDYTLVEDNDNDWYLRSGEVTTPSPDPDPPTPDPPTPDPPTPEPTPAY 950
Qy 269 IVTVNGHIDPNSKGDLLRLSTLYGYNSTIWRSMWDNEVAFNNGSGSGDG 319
Db 951 QPVLNAKVG-----GYLNNLRAANQAFME--RDHAGGDG 984

RESULT 14
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AC P16271;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P1-type proteinase precursor (EC 3.4.21.-) (Wall-associated serine
DE proteinase).
GN PRTP.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OG Plasmid pmv05.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_Taxid=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WG2;
RX MEDLINE=88149035; PubMed=3278687;
RA Kok J., Leenhouts K.J., Haandrikman A.J., Ledebor A.M., Venema G.;
RT "Nucleotide sequence of the cell wall proteinase gene of
RT Streptococcus cremoris WG2.";
RL Appl. Environ. Microbiol. 54:231-238(1988).
CC -1- FUNCTION OF THE BACTERIA BREAKS DOWN MILK PROTEINS DURING THE
CC GROWTH OF THE BACTERIA ON MILK.
CC -1- CATALYTIC ACTIVITY: Endopeptidase activity with very broad
CC specificity, although some subsite preference have been noted,
CC e.g. large hydrophobic residues in the P1 and P4 positions, and
CC Pro in the P2 position. Best known for its action on caseins,
CC although it has been shown to hydrolyze hemoglobin and oxidized
CC insulin B-chain.
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (potential).
CC -1- SIMILARITY: Belongs to peptidase family S8.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M24767; AAA17677.1; -
DR HSSP; P00782; 1S01.
DR MEROPS; S08.019; -
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003137; PA.
DR InterPro; IPR000209; Peptidase_S8.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02225; PA; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR TIGRFAms; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
RL

KW Hydrolyase; Serine protease; Cell wall; Peptidoglycan-anchor; Zymogen;
KM Signal; Plasmid.
FT SIGNAL 1 33
FT PROPEP 34 187
FT CHAIN 188 1870
FT PROPEP 1871 1902
FT ACT_SITE 217 217
FT ACT_SITE 281 281
FT ACT_SITE 620 620
FT SITE 1867 1871
FT MOD_RES 1870 1870
SQ SEQUENCE 1902 AA; 199910 MW; 2901C7F19B2E5D0B CRC64;
Query Match 6.6%; Score 113.5; DB 1; Length 1902;
Best Local Similarity 21.1%; Pred. No. 30;
Matches 71; Conservative 35; Mismatches 100; Indels 131; Gaps 14;

Qy 3 AADAPAGTDITNQ-----LTNVTGIDSGT-----TVYPHAGYVKL- 40
Db 506 AQAAGAGLITVNDGTATPVTSMALTTFTPTFGLSSVTGQKLVDPVTAHPDDSLGVKIA 565
Qy 41 -----NYGFSVPNSAVKGDFTKITVP-----KELNLNGVTS--TAK 74
Db 566 LTLVPNQKYTEDKMSDFTSYG-PVSNLSFRPD---ITAPGGINWSTQNNGYTNMSGTSM 621
Qy 75 VPPIMAGDQVLANGVIDSDGNVITYF-----TDYVNTKDYKATLTMPAYIDPENV 125
Db 622 ASPFIAGSQAALKQALNNKNPNFYAYYKQLKGTALTDFLKT-----VENMTA 668
Qy 126 KKTGNVTLATGIGSTTANKTVLVDEYKGYKFNLSIKGTIDQIDK----- 170
Db 669 QPINDINYNNTIVSPRRQAGLVD-----VKAIDALENPSTVVAENGYPAVE 717
Qy 171 -----TNNTYRQTIYVNSGDNVIAPLVTGNLKPNTDSNAL----IDQNTSISKYKVD 220
Db 718 LKDFSTDKTFKLT-----TNSTTHELTYYQMSDNTDTNAVYTSATDPNSGVLYDKKID 771
Qy 221 NAADISESYFVNPEDEVTNSVNTFPNPNOYKEF 257
Db 772 GAA-----IKAGSNITVPAGKTAQIEF 793

RESULT 15
P2P_LACPA STANDARD; PRT; 1902 AA.
ID P2P_LACPA
AC Q02470;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P11-type proteinase precursor (EC 3.4.21.96) (Lactocepin) (Cell wall-
DE associated serine proteinase) (LP151).
GN PRTP.
OS Lactobacillus paracasei.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_Taxid=1597;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCDO 151;
RX MEDLINE=92381481; PubMed=1512565;
RA Holck A., Naes H.;
RT "Cloning, sequencing and expression of the gene encoding the cell-
RT envelope-associated proteinase from Lactobacillus paracasei subsp.
RT paracasei NCDO 151.";
RL J. Gen. Microbiol. 138:1353-1364(1992).
RN [2]
RP SEQUENCE OF 189-196.
RX MEDLINE=92226694; PubMed=1564442;
RA Naes H., Nissen-Meyer J.;
RT "Purification and N-terminal amino acid sequence determination of the
RT cell-wall-bound proteinase from Lactobacillus paracasei subsp.
RT paracasei.";
RL J. Gen. Microbiol. 138:313-318(1992).
RL

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OM protein - protein search, using sw model

Run on: March 26, 2004, 05:07:57 ; Search time 1044.06 Seconds
(without alignments)
82.955 Million cell updates/sec

Title: US-10-056-052A-4
Perfect score: 1732
Sequence: 1 MVAADAPAGTDTITNQLTNV.....NGSGSGDGIDKRVVPEQPDF 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1732	100.0	331	US-10-056-052-4	Sequence 4, Appli
2	1732	100.0	345	US-09-813-820-7	Sequence 7, Appli
3	1727	99.7	520	US-10-056-052-2	Sequence 2, Appli
4	1723	99.5	936	US-08-781-986A-5249	Sequence 5249, Ap
5	1723	99.5	936	US-10-329-624-5249	Sequence 5249, Ap
6	1518	87.6	1021	US-09-815-242-5471	Sequence 5471, Ap
7	1518	87.6	1021	US-09-815-242-12544	Sequence 12544, A
8	1517	87.6	935	US-10-282-122A-44326	Sequence 44326, A
9	1433	82.7	496	US-10-311-879-29	Sequence 29, Appli
10	416.5	24.0	961	US-10-282-122A-43778	Sequence 43778, A
11	409	23.6	767	US-09-815-242-5899	Sequence 5899, Ap
12	409	23.6	767	US-09-815-242-13140	Sequence 13140, A
13	353	20.4	343	US-10-378-674-4	Sequence 4, Appli
14	353	20.4	560	US-10-378-674-2	Sequence 2, Appli
15	353	20.4	892	US-10-282-122A-70481	Sequence 70481, A

16	353	20.4	930	12	US-10-615-383-10	Sequence 10, Appli
17	349	20.2	549	15	US-10-378-674-9	Sequence 9, Appli
18	349	20.2	1092	15	US-10-378-674-8	Sequence 8, Appli
19	346	20.0	978	9	US-09-815-242-5456	Sequence 5456, Ap
20	346	20.0	1001	9	US-09-815-242-12686	Sequence 12686, A
21	339	19.6	1018	9	US-09-815-242-5797	Sequence 5797, Ap
22	339	19.6	1018	9	US-09-815-242-12838	Sequence 12838, A
23	331	19.1	1027	8	US-08-781-986A-5254	Sequence 5254, Ap
24	331	19.1	1027	12	US-10-329-624-5254	Sequence 5254, Ap
25	324.5	18.7	1038	12	US-10-282-122A-43827	Sequence 43827, A
26	320.5	18.5	1141	12	US-10-282-122A-70251	Sequence 70251, A
27	312.5	18.0	877	12	US-10-282-122A-70428	Sequence 70428, A
28	304.5	17.6	316	15	US-10-378-674-6	Sequence 6, Appli
29	282.5	16.3	251	8	US-08-781-986A-5252	Sequence 5252, Ap
30	282.5	16.3	251	12	US-10-329-624-5252	Sequence 5252, Ap
31	257.5	14.9	1349	9	US-09-815-242-5898	Sequence 5898, Ap
32	257.5	14.9	1349	9	US-09-815-242-13137	Sequence 13137, A
33	240.5	13.9	1385	12	US-10-282-122A-44324	Sequence 44324, A
34	232.5	13.4	932	9	US-09-815-242-5578	Sequence 5578, Ap
35	232.5	13.4	932	9	US-09-815-242-12438	Sequence 12438, A
36	229.5	13.3	953	12	US-10-282-122A-44457	Sequence 44457, A
37	212.5	12.3	1920	12	US-10-282-122A-71413	Sequence 71413, A
38	210.5	12.2	841	9	US-09-815-242-5779	Sequence 5779, Ap
39	210.5	12.2	841	9	US-09-815-242-12751	Sequence 12751, A
40	201.5	11.6	1633	12	US-10-282-122A-70437	Sequence 70437, A
41	201.5	11.6	1742	12	US-10-615-383-4	Sequence 4, Appli
42	187.5	10.8	670	12	US-10-282-122A-70444	Sequence 70444, A
43	140	8.1	2060	15	US-10-381-596A-2	Sequence 2, Appli
44	139.5	8.0	628	12	US-10-282-122A-57384	Sequence 57384, A
45	139	8.0	3930	12	US-10-282-122A-46817	Sequence 46817, A

ALIGNMENTS

RESULT 1
US-10-056-052-4
; Sequence 4, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056, 052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308, 116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298, 413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274, 611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264, 072
; PRIOR FILING DATE: 2001-01-26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-4

Query Match 100.0%; Score 1732; DB 14; Length 331;
Best Local Similarity 100.0%; Pred. No. 9.6e-139;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MVAADAPAGTDTITNQLTNVYVGIDSGTTPYHQAQYVYKLVNGFSVPNSAVKGDPTKITV 60

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DB 61 PKELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFSTDYVNTKDVKATLTMPAYI 120
QY 121 DPENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIY 180
DB 121 DPENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIY 180
QY 181 VNPSGDNVIAPVLTGNLKPNTDSNALIDQNTSISKYKVDNAADLSESYFVNPFEDVT 240
DB 181 VNPSGDNVIAPVLTGNLKPNTDSNALIDQNTSISKYKVDNAADLSESYFVNPFEDVT 240
QY 241 NSVNTTFPNPNOYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGYNSTIWR 300
DB 241 NSVNTTFPNPNOYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGYNSTIWR 300
QY 301 SMSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 331
DB 301 SMSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 331

RESULT 2

US-09-813-820-7
Sequence 7, Application US/09813820
Patent No. US20020102262A1

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
Patti, Joseph M.
House-Pompeo, Karen
Shanham, Narayana
Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,820
FILING DATE: 22-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,253
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAWK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

US-09-813-820-7
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Query Match 100.0%; Score 1732; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 1e-138;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PKELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFSTDYVNTKDVKATLTMPAYI 120
DB 73 PKELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFSTDYVNTKDVKATLTMPAYI 132
QY 121 DPENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIY 180
DB 133 DPENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIY 192
QY 181 VNPSGDNVIAPVLTGNLKPNTDSNALIDQNTSISKYKVDNAADLSESYFVNPFEDVT 240
DB 193 VNPSGDNVIAPVLTGNLKPNTDSNALIDQNTSISKYKVDNAADLSESYFVNPFEDVT 252
QY 241 NSVNTTFPNPNOYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGYNSTIWR 300
DB 253 NSVNTTFPNPNOYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGYNSTIWR 312
QY 301 SMSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 331
DB 313 SMSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 343

RESULT 3

US-10-056-052-2
Sequence 2, Application US/10056052
Publication No. US20030099656A1

GENERAL INFORMATION:

APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALI, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/274,611
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/264,072
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 520
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-056-052-2

Query Match 99.7%; Score 1727; DB 14; Length 520;
Best Local Similarity 100.0%; Pred. No. 5e-138;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAADAPAGTDITNQLTNVTGIDSGTTVYPHAGYVKLNYSFVPSNAVKGDTFKITV 61
DB 182 VAADAPAGTDITNQLTNVTGIDSGTTVYPHAGYVKLNYSFVPSNAVKGDTFKITV 241
QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFSTDYVNTKDVKATLTMPAYI 121
DB 242 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFSTDYVNTKDVKATLTMPAYI 301
QY 122 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIY 181
DB 302 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIY 361
QY 182 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSISKYKVDNAADLSESYFVNPFEDVTN 241

Db 362 NPSGDNVIAFVLITGNLKPNTDSNALIDQNTSIKVKVDNAADLSESYFVNPFEDVTN 421
QY 242 SVNITFPNPNOYKYEFNTPDDQITTPYIVVYNGHIDPNSKGDALRSTLYGNSNIWRS 301
Db 422 SVNITFPNPNOYKYEFNTPDDQITTPYIVVYNGHIDPNSKGDALRSTLYGNSNIWRS 481
QY 302 MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 331
Db 482 MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 511

RESULT 4

US-08-781-986A-5249
; Sequence 5249, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5249

Query Match 99.5%; Score 1723; DB 8; Length 936;
Best Local Similarity 99.7%; Pred. No. 2.6e-137;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNQLTNVTYVGIDSGTTVPYPHQAGYVKLNYGFSVPNSAVKGDTFKITVP 61
Db 230 VAADAPVAGTDTITNQLTNVTYVGIDSGTTVPYPHQAGYVKLNYGFSVPNSAVKGDTFKITVP 289
QY 62 KEINLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVITYTFTDYVNTKDDVKATLTMPAYID 121
Db 290 KEINLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVITYTFTDYVNTKDDVKATLTMPAYID 349
QY 122 PENYKKTGNVTLATIGISTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 181
Db 350 PENYKKTGNVTLATIGISTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 409
QY 182 NPSGDNVIAFVLITGNLKPNTDSNALIDQNTSIKVKVDNAADLSESYFVNPFEDVTN 241
Db 410 NPSGDNVIAFVLITGNLKPNTDSNALIDQNTSIKVKVDNAADLSESYFVNPFEDVTN 469

QY 242 SVNITFPNPNOYKYEFNTPDDQITTPYIVVYNGHIDPNSKGDALRSTLYGNSNIWRS 301
Db 470 SVNITFPNPNOYKYEFNTPDDQITTPYIVVYNGHIDPNSKGDALRSTLYGNSNIWRS 529
QY 302 MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 331
Db 530 MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 559

RESULT 5

US-10-329-624-5249
; Sequence 5249, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5249:
US-10-329-624-5249

Query Match 99.5%; Score 1723; DB 12; Length 936;
Best Local Similarity 99.7%; Pred. No. 2.6e-137;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNQLTNVTYVGIDSGTTVPYPHQAGYVKLNYGFSVPNSAVKGDTFKITVP 61
Db 230 VAADAPVAGTDTITNQLTNVTYVGIDSGTTVPYPHQAGYVKLNYGFSVPNSAVKGDTFKITVP 289
QY 62 KEINLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVITYTFTDYVNTKDDVKATLTMPAYID 121
Db 290 KEINLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVITYTFTDYVNTKDDVKATLTMPAYID 349

QY	122	PENYKKTGNVTLATIGISTTANKIYLVDEYKYGKFFYNLSIKGTIDQIDKTNNTYRQTIYV	181
Db	350	PENYKKTGNVTLATIGISTTANKIYLVDEYKYGKFFYNLSIKGTIDQIDKTNNTYRQTIYV	409
QY	182	NPSGDNYIAPVLTGNLKPNTSDSNALIDQNTSIKVVYKVDNADLSESYFVNPFNEFDVTN	241
Db	410	NPSGDNYIAPVLTGNLKPNTSDSNALIDQNTSIKVVYKVDNADLSESYFVNPFNEFDVTN	469
QY	242	SVNITFPENQYKVEFNTPPDDQITTPYIIVVNGHIDPNSKGLALRSTLYGYNNSNIWRS	301
Db	470	SVNITFPENQYKVEFNTPPDDQITTPYIIVVNGHIDPNSKGLALRSTLYGYNNSNIWRS	529
QY	302	MSWDNEVAFFNNGSGSGDGIDKPVVPEQDPE	331
Db	530	MSWDNEVAFFNNGSGSGDGIDKPVVPEQDPE	559

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RESULT 6
US-09-815-242-5471
; Sequence 5471, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5471
; LENGTH: 1021
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5471

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Query Match	87.6%;	Score 1518;	DB 9;	Length 1021;
Best Local Similarity	87.3%;	Pred. No. 7.6e-120;		
Matches 288;	Conservative 17;	Mismatches 25;	Indels 0;	Gaps 0;

[illegible]

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QY      182 NPSGDNVIAPVLTGNLKPNTDSNALIDQÖNTSİKVKYKVDNAADLSESİYFVNPEMEDVTN 241
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      401 NPSGDNVLPALTGNLIPNTXSNALIDAKNTDİKVKRYVDNANDLSESIYVNPSEDEDTN 460

QY      242 SVNITFENPNQYKVEFNTPPDQİTTPIYIVVNGHIDPNSKGDLLRSTLYGYSNNTIWR 301
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      461 QVRISFENANQYKVEFPTDDQİTTPIYIVVNGHIDPASTGDLALRSTFYGYDSNFIWR 520

QY      302 MSWDNEVAFNNGSGSGDGDİKPYVPEQPD 331
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      521 MSWDNEVAFNNGSGSGDGDİKPYVPEQPD 550

```

```

RESULT 7
US-09-815-242-12544
: Sequence 12544, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsern, Kari L.
: APPLICANT: Zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Ess
: TITLE OF INVENTION: Prokaryotes
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12544
: LENGTH: 1021
: TYPE: PRT
: ORGANISM: Staphylococcus aureus
US-09-815-242-12544

```

Query Match	87.6%;	Score 1518;	DB 9;	Length 1021;
Best Local Similarity	87.3%;	Pred. No. 7.6e-120;		
Matches 288;	Conservative 17;	Mismatches 25;	Indels 0;	Gaps 0;

[illegible]

QY	242	SVNITFENPNQYKVEFNTPDDQTTPYIVVNVNGHIDPNSKGIDLALRSTLYGYNISNIITWRS	301
	:		:
Db	461	QVRISFPANQYKVEFTPTDDQTTPYIVVNVNGHIDPASTGLALRSTFYGYDSNFITWRS	520
QY	302	MSWDNEVAFFNNSGSGGDGI DKPVVPPEQDE	331
	:		:
Db	521	MSWDNEVAFFNNSGSGGDGI DKPVVPPEQDE	550

```

RESULT 8
US-10-282-122A-44326
; Sequence 44326, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44326.
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-44326

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Query Match          87.6%; Score 1517; DB 12; Length 935;
Best Local Similarity 87.3%; Pred. No. 8.1e-120;
Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0
QY      2  VAADAPAGDTITNQLTNVTVGIDSGTIVYPHOAGYVKLNNGFSVPNSAVKGDTEKITVP 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      221 VAADAPAGDTITNQLTDPVKVTIDSGTIVYPHOAGYVKLNNGFSVPNSAVKGDTEKITVP 280
QY      62  KELNLNGVISTAKVPPIMAGDQVLANGVIDSDGNVIYFTFDYVNTKDKDYKATLLTMPAYID 121
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      281 KELNLNGVISTAKVPPIMAGDQVLANGVIDSDGNVIYFTFDYVDNKENENTANITMPAYID 340
QY      122 PENVKKTGNVTLATGIGSTTANKTVLVDIYEKYEKFYNLSIKGTIDQIDKNNNTYRQTIYV 181

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Db	341	PEWVTKGNVTLTTGTGINTASKTVLIDIEKYGGCFHNLSIKGTIDQIDKTNNTYRQTIYV	400
QY	182	NPSGDNVIAFVLTKNLKPNIDSNALIDQÖNTSIRKYKYDNAADLSES*YFVNPEPNEDEVTN	241
Db	401	NPSGDNVLLPALTGNLIPNTKSNALIDAKNTIDIKYRVNDNANDLSESYVNPSPDEVDTN	460
QY	242	SVNITFEPNPNQYKVEFNTPEDDQITTPYIVVYNGHIDPNSKGDLLALRSTLYGYSNIIWRS	301
Db	461	QVRISFEPNANQYKVEFPITDDQITTPYIVVYNGHIDPASTGDLALRSTFYGYDSNFIWRS	520
QY	302	MSWDNEVAFFNNGSGSGDGIDKPVVPEQPDE	331
Db	521	MSWDNEVAFFNNGSGSGDGIDKPVVPEQPDE	550

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RESULT 9
US-10-311-879-29
; Sequence 29, Application US/10311879
; Publication No. US20030186275A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; TITLE OF INVENTION: Antigenic Peptides
; FILE REFERENCE: tox1n
; CURRENT APPLICATION NUMBER: US/10/311,879
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-311-879-29

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Query Match	82.7%;	Score 1433;	DB 14;	Length 496;
Best Local Similarity	100.0%;	Pred. No. 4.3e-113;		
Matches 276;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2	VAADAPAGATDITNQLTNTVTVGIDSGTTVYPHOAGYVXLNNGFSVPNSAVKGDTEKITVP	61	
DB	221	VAADAPAGATDITNQLTNTVTVGIDSGTTVYPHOAGYVXLNNGFSVPNSAVKGDTEKITVP	280	
QY	62	KELNUNGVSTAKVPPIMAGQVLANGVIDSDGNVIYTFEDYVNTKDDVKATLTMPAYID	121	
DB	281	KELNUNGVSTAKVPPIMAGQVLANGVIDSDGNVIYTFEDYVNTKDDVKATLTMPAYID	340	
QY	122	PENVKKTGNVTLATIGISTANKTVLVDEYKYGKFYNLSIKGTIDQIDKTNNTYRQTIYV	181	
DB	341	PENVKKTGNVTLATIGISTANKTVLVDEYKYGKFYNLSIKGTIDQIDKTNNTYRQTIYV	400	
QY	182	NPSGDNVIAPVLTGNLKPNTDSNALIDQQNTSIKVKYKVDAADLSESYFVNPENFEDVTN	241	
DB	401	NPSGDNVIAPVLTGNLKPNTDSNALIDQQNTSIKVKYKVDAADLSESYFVNPENFEDVTN	460	
QY	242	SVNITPENPNQYKVEFNTPEDQITTPYIVVNGHID	277	
DB	461	SVNITPENPNQYKVEFNTPEDQITTPYIVVNGHID	496	

RESULT 10
US-10-282-122A-43778
; Sequence 43778, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant


```

; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43778
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-43778

```

[illegible]

```

; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5899
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-015-242-5899

```

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Query Match      23.6%; Score 409; DB 9; Length 767;
Best Local Similarity 28.9%; Pred. No. 7,7e-26;
Matches 101; Conservative 72; Mismatches 131; Indels 46; Gaps 11;

QY      2 VAADAPAGIDITNQLTNVTVGIDSGT-----TVYPHQAGYVKLNYGFSVPSNAV 51
      | : ||| : ||| : : : : | : : | : | : | : | :
DB      155 VVEETKATGTDVYTNK-----VEVEEGSEIVGHKQDTNVVNPNAERVTLTKYKWKFGEGIK 209
      | : | : | : | : | : | : | : | : | : | : | :
QY      52 KGDTPKITVPKELNNGVSTAKVPPIMAGD-QVLANGVIDSDGNVITYFTDYVNTKDDV 110
      | | : : : : : : : | : | : | : | : | : | : | :
DB      210 AGDYFDFTLSDNVETHGISLTKRVPKIKSTIDGQVMAIGEIIIGERKVRYTEKEVQEKDIL 269
      | : | : | : | : | : | : | : | : | : | : | :
QY      111 KATLTPAYIDPENYKKTGNVTLATIGSTTANKVLVDY-----EKYGFYNLSIKGTI 165
      | : : : : | : | : | : | : | : | : | : | : | :
DB      270 TAEISLNLFIIDFTVYQKGNQNVKLGETTTSKIFINIQYLGVRDNWG---VTANGRI 325
      | : : : : | : | : | : | : | : | : | : | : | :
QY      166 DQIDKTNNTYRQTIYVNPBGDNVIAFVLTSNL---KPNLDSNALIDQNTSIKVKYKVDN 221
      | : : : : : : : : : : : : : : : : : : : : :
DB      326 DTLNKVDGKFSHFAYKPKPNQSLSSVTVTGQVTKGNKPGVN-----NPTVKVYKHIG 377
      | : : : : : : : : : : : : : : : : : : : : :
QY      222 AADLSESYFVNPNEN---FEDVTVNSVNITFPNPNQYKVEFNTPPDQITTPYIVVNGHIDP 278
      | : | : | : : : : | : | : | : | : | : | : | :
DB      378 SDDLAEISVYAKLIDVSKFEDVTDNMSLDFDTNGGYSLEFNNDQ--SKNYVIKIEGYIDS 435
      | : | : | : : : : | : | : | : | : | : | : | :
QY      279 NSKGDLALRSTLYGINSNIIRWSMSWDNEVAFNNGSGSGDGDIDK--PVV 325
      | : : | : : : : : : : : : : : : : : : : : :
DB      436 NA-SNLEFQTHLFGYNYYYTSTNLTWKNGVAFYSNNAQGGDKDKLKEPII 484
      | : : | : : : : : : : : : : : : : : : : : :

RESULT 12
US-09-815-242-13140
; Sequence 13140, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.

```

```

: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: TITLE OF INVENTION: Prokaryotes
: FILE REFERENCE: ELITRA.01A
: CURRENT APPLICATION NUMBER: US/09/815,242
: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 13140
: LENGTH: 767
: TYPE: PRT
: ORGANISM: Staphylococcus aureus
US-09-815-242-13140

```

Query Match	23.6%	Score 409;	DB 9;	Length 767;
Best Local Similarity	28.9%;	Pred. No. 7.7e-26;		
Matches 101;	Conservative 72;	Mismatches 131;	Indels 46;	Gaps 11;

[illegible]

```

RESULT 13
US-10-378-674-4
; Sequence 4, Application US/10378674
; Publication No. US20040006209A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATIVE
; TITLE OF INVENTION: STAPHYLOCOCCAL PROTEINS
; FILE REFERENCE: P07556US01/BAS
; CURRENT APPLICATION NUMBER: US/10/378,674
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/361,324
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

```

```

; LENGTH: 343
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-4

```

Query Match	20.4%	Score 353;	DB 15;	Length 343;
Best Local Similarity	30.6%;	Pred. No. 1.3e-21;		
Matches 101; Conservative	60;	Mismatches 139;	Indels 30;	Gaps 14;

```

QY      13 ITHQLTNVTVGI-DSGTTYYPHQAGYVKLANGESVPNSAVKGDTEKLTVPKELNLNGVTS 71
Db      30 VTDQ--SITEGYDDSDGIIKAHDAENLIYDVFPEVDDKVKSGDITMYNIDKNTVPSDLTD 87
QY      72 TAKYEPIMAGD-QVLANGVID-SDGNVITYTFIDYVNTKDDVKATLTMEAYIDPENVKYKTG 129
Db      88 SFAIPKIKDNGSEIATGYDNTNKQITLYTFIDYVDKYENIKAHKLKLTYSIDKSKVPNNN 147
QY      130 --NVTLATIGSTTANKTVLVDYEKGYKFXNLSIKGTIDQIDKTNNTYRQTIYVNPSCD 186
Db      148 TKLDVEYKKTALSS--VNKXITVEYQKPNENRNTANLQSMFTNIDITKHTVEQTIYINPL-- 203
QY      187 NVIAEVLGTNLKPNTDSNALIDQCNTSIKVKYKVDNAAADLSESYFV--NEENFEDVTSVNI 245
Db      204 RYSAKETNWNISGNGDEGSTIIDSTIIKVKYKVDNQNLPDSNRIFYDSEYEDVTNDIDYA 263
QY      246 TFPNPQYKVEFNTPPDQITTPYIVVYNGHIDBNSKGD-----LALRSTLYGYSNII 298
Db      264 QLGNNNDVNINFG---NIDSPYIIKVIKSKYDPN--KDDYTTIIQQTVMQOTTINEYTG-- 316
QY      299 WRSMWMDNEVAFNNGSGSGGIDKRPVPEQ 328
Db      317 FRTASVDNTIAFSTSSGGQGG-DLP--PEK 343

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RESULT 14
US-10-378

```

; Sequence 2, Application US/10378674
; Publication No. US20040006209A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATIV
; TITLE OF INVENTION: STAPHYLOCOCCAL PROTEINS
; FILE REFERENCE: P07556US01/BAS
; CURRENT APPLICATION NUMBER: US/10/378,674
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/361,324
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-2

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Query Match	20.4%	Score 353;	DB 15;	Length 560;
Best Local Similarity	30.6%	Pred. No. 2.8e-21;		
Matches 101; Conservative	60;	Mismatches 139;	Indels 30;	Gaps 14;

```

QY      13 ITNOLNTVTGI-DSGTTYVPHQAGYVKLNIGSPVNSAVKGDTEFKITVEKELNLNGVTS  71
      :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db      247 VTDQ--SITEGYDDSGIIRAKHAENLIYDVTFEYVDKVKSGDGMTVINIDKNTPPSDLTD  304

QY      72 TAKVPPIMAGD-QVLANGVID-SDGNVIYTFPTYVNTKDDVKATLTMPAYIDPENVKKTG  129
      :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db      305 SFAIPKIKNSGEIITATGYDMNTNKQITYTFPTYVDKYENIKAKHLKLTSYIDKSKVPNNN  364

QY      130 ---NVLATGIGSTTANKTVLVDEYKYGKFFYNLSIKGTIDQIDKTNNTYROTIIYVNPSCD  186
      :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db      365 TKLDVEYKTA LSS--VNKTIIVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPL--  420

QY      187 NVLIAPVLIGNLKPNTDSNALIDQNTSIIKVYKVDAADLSESYFV-NPENEDVTVNSVNI  245
      | :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:

```

Db 421 RYSAKETNVNISGNDEGSTIIDSTIIKVKVGDNONLPDSNRIDYSEYEDVTNDDYA 480
QY 246 TFPENQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGD-----LALRSTLYGYSNII 298
Db 481 QLGNNNDVNINFG---NIDSPYIIKVISKYDPN-KDDYTTIIQQTVMQTTINEYTGE-- 533
QY 299 WRSMSWDNEVAFNNGSGSGDIDKPVVPEQ 328
Db 534 FRTASYDNNTIAFSTSSGQGQ-DLP--PEK 560

RESULT 15
US-10-282-122A-70481
; Sequence 70481, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70481
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70481

Query Match 20.4%; Score 353; DB 12; Length 892;
Best Local Similarity 30.6%; Pred. No. 5.5e-21;
Matches 101; Conservative 60; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLTNTVGI-DSGTTVYPHAGYVYKLVGFSVPNSAVKGDFTFKITVPKELNLNGVTS 71
Db 246 VTDQ--SITEGYDSDGIIKAHDAENLYDYTFEVDKVKSGDFTVNIDKNTVPSDLTD 303
QY 72 TAKVPPIMAGD-QVLANGVID-SDGNVITYFTFDYVNTKDDVKATLTMFAYIDPENVKKTG 129
Db 304 SFAIPKIKDNGSEIATGTVDNTNKQITTYTFTDYVDKYENIKAHKLKLTSYIDKSKVPNNN 363

QY 130 ---NYTLATIGSTTANKYLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYVNPSCD 186
Db 364 TKLDVEYKTAISS--VNKTIVYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPL-- 419
QY 187 NVIAPVLTGNLKPNTDSNALIDQONTSIKVKYKVDNAADLSESYFV-NPENFEDVTSVNI 245
Db 420 RYSAKETNVNISGNDEGSTIIDSTIIKVKVGDNONLPDSNRIDYSEYEDVTNDDYA 479
QY 246 TFPENQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGD-----LALRSTLYGYSNII 298
Db 480 QLGNNNDVNINFG---NIDSPYIIKVISKYDPN-KDDYTTIIQQTVMQTTINEYTGE-- 532
QY 299 WRSMSWDNEVAFNNGSGSGDIDKPVVPEQ 328
Db 533 FRTASYDNNTIAFSTSSGQGQ-DLP--PEK 559

Search completed: March 26, 2004, 05:53:03
Job time : 1086.06 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:17 ; Search time 34.039 Seconds
(without alignments)
935.380 Million cell updates/sec

Title: US-10-056-052A-4
Perfect score: 1732
Sequence: 1 MVAADAPAPAGTDITNQLTNV.....NGSGSGDGIDKPVPEQPD 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1727	99.7	933	2	S41539	fibrinogen-binding
2	1517	87.6	989	2	D89852	fibrinogen-binding
3	416.5	24.0	961	2	G90053	hypothetical prote
4	409	23.6	940	2	S19702	fibrinectin-binding
5	349	20.2	1092	2	T30214	fibrinogen-binding
6	331	19.1	1018	2	A32192	fibrinectin-binding
7	324.5	18.7	1038	2	H90053	hypothetical prote
8	323.5	18.7	1166	2	T28680	fibrinogen-binding
9	320.5	18.5	1141	2	E89824	hypothetical prote
10	312.5	18.0	877	2	F90070	clumping factor B
11	257.5	14.9	1315	2	T28679	fibrinogen-binding
12	240.5	13.9	1385	2	D89824	hypothetical prote
13	229.5	13.3	953	2	C89824	hypothetical prote
14	182	10.5	1039	2	T30856	protein F2 - Strep
15	161.5	9.3	463	2	AG1542	wall associated pr
16	157.5	9.1	462	2	AH1184	wall associated pr
17	147.5	8.5	586	2	AD1458	probable peptidogl
18	141	8.1	1386	2	AC1533	surface protein (l
19	137	7.9	439	2	AE1251	probable peptidogl
20	137	7.9	4152	2	T31102	filamentous hemagg
21	135	7.8	1983	2	G86643	hypothetical prote
22	132.5	7.7	1457	2	D81019	adhesion and penet
23	132	7.6	1449	2	B81963	IGA-specific serin
24	129	7.4	762	2	A34355	cell surface prote
25	128	7.4	1158	2	AF1852	hypothetical prote
26	128	7.4	2021	2	A97859	190-KDa cell surfa
27	127	7.3	642	2	D81401	probable flagellar
28	127	7.3	793	2	AH1094	probable peptidogl
29	126.5	7.3	571	2	AI1094	probable peptidogl

30	126.5	7.3	1029	2	T30852	outer membrane pro
31	124.5	7.2	1039	2	D97985	hypothetical prote
32	123.5	7.1	1417	2	AG2137	hypothetical prote
33	122.5	7.1	657	2	AD1525	probable cell surf
34	122.5	7.1	1039	2	H95115	conserved hypothet
35	122.5	7.1	1487	2	AG2560	hypothetical prote
36	122	7.0	1578	2	AD1512	peptidoglycan bou
37	121.5	7.0	2249	2	A41477	190K surface antig
38	121.5	7.0	3890	2	C89921	hypothetical prote
39	121	7.0	1910	2	AF0394	probable adhesin h
40	119.5	6.9	691	2	B75622	hypothetical prote
41	119.5	6.9	836	2	D97182	extracellular neut
42	118.5	6.8	749	2	E86774	hypothetical prote
43	118.5	6.8	1369	2	T17504	hypothetical prote
44	118	6.8	1873	2	T30944	surface protein pr
45	117.5	6.8	449	2	JC7306	extracellular prot

ALIGNMENTS

RESULT 1
S41539
fibrinogen-binding protein - Staphylococcus aureus
N:Alternate names: clumping factor
C:Species: Staphylococcus aureus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999
C/Accession: S41539; S36630
R:McDevitt, D.; Francois, P.; Vaudaux, P.; Foster, T.J.
Mol. Microbiol. 11, 237-248, 1994
A>Title: Molecular characterization of the clumping factor (fibrinogen receptor) of Staphylococcus aureus
A/Reference number: S41539; MUID:94224142; PMID:8170386
A/Accession: S41539
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-933 <MCD>
A/Cross-references: EMBL:Z18852; NID:g397525; PIDN:CAA79304.1; PID:g397526

Query Match 99.7%; Score 1727; DB 2; Length 933;
Best Local Similarity 100.0%; Pred. No. 1e-99;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	VAADAPAPAGTDITNQLTNVTVGIDSGTTVPYHQAGYVKLNYGFSVPNSAYKGDITFKITVP	61
DB	221	VAADAPAPAGTDITNQLTNVTVGIDSGTTVPYHQAGYVKLNYGFSVPNSAYKGDITFKITVP	280
QY	62	KEINLVGTSTAKVPPIAGDQVLANGVIDSDGNVYFTDYNTKDVKATLTMPAYID	121
DB	281	KEINLVGTSTAKVPPIAGDQVLANGVIDSDGNVYFTDYNTKDVKATLTMPAYID	340
QY	122	PENVKKTGNVTLATGISTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV	181
DB	341	PENVKKTGNVTLATGISTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV	400
QY	182	NPSGDNVIAPVLTGNLKPNVDSNALIDQONTSIKVKYKVNAAADLSESYFVNPNEDVTN	241
DB	401	NPSGDNVIAPVLTGNLKPNVDSNALIDQONTSIKVKYKVNAAADLSESYFVNPNEDVTN	460
QY	242	SVNITFPNNGYKVEFNTPDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIWRS	301
DB	461	SVNITFPNNGYKVEFNTPDQITTPYIVVNGHIDPNSKGLALRSTLYGNSNIWRS	520
QY	302	MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 331	
DB	521	MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 550	

RESULT 2
D89852
fibrinogen-binding protein A, clumping factor [imported] - Staphylococcus aureus (strain
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: D89852

R.;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: D89852

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-989 <KUR>

A;Cross-references: GB:BA000018; PID:g13700678; PIDN:BAB41975.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:

A;Gene: c1fa

Query Match 87.6%; Score 1517; DB 2; Length 989;

Best Local Similarity 87.3%; Pred. No. 1.3e-86;

Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 VAADAPAAAGTDTITNQLTNVTGIDSGTTVPHQAGYVKLVGFSVPNSAVKGDTEKITVP 61

DB 221 VAADAPAAAGTDTITNQLTDVKVTIDSGTTVPHQAGYVKLVGFSVPNSAVKGDTEKITVP 280

QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFDYVNTKDVKATLTMPAYID 121

DB 281 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFDYVNTKENVNTANITMPAYID 340

QY 122 PENVKKTKGNVTLATIGSTTANKTVLVDEYKGFYNLSIKGTIDQIDKTNNTYRQITIV 181

DB 341 PENVKKTKGNVTLTIGTIGTNTASKTVLIDYEKGFHNLISIKGTIDQIDKTNNTYRQITIV 400

QY 182 NPSGDNVIAVPLTGNLKPNTDSNALIDQNTSIKVKVDNAADLSESYFVNPNFEDVTN 241

DB 401 NPSGDNVIAVPLTGNLIPNTKSNALIDAKNTDIKVRVDNANDLSESYFVNPNFEDVTN 460

QY 242 SVNITFPNPQYKVEFNTPDDQITTPYIVVNGHIDPNKSGDLALRSTLYGNSNIWES 301

DB 461 QVRISFPNANQYKVEFTDDQITTPYIVVNGHIDPASTGDLALRSTFYGYDSNFIWES 520

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

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DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 302 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 331

DB 521 MSWDNEVAFNNGSGSGDIDKPVVPEQPD 550

QY 58 ITVPEKELNLNGVTSTAKVPPIMAG--DQVLANGVIDSDGNVIYTFDYVNTKDVKATLT 115

DB 218 FTLSDNVETHGISTLRKPEIKSSTEDKVMANGVINERTIRYFTDYINMKDLTAELN 277

QY 116 MPAYIDPENVKKTGNVTLATIGSTTANKTVLVY-----EYKGFYNLSIKGTIDQIDK 170

DB 278 INLFIDPTVTQKGSQKVEVTLGQNKVSKEFDIKLVDGKDRMG---VTNGRIDTLNK 333

QY 171 TNNTYRQITIVNPSGDNVIAVPLTGNLKPNTDSNALIDQNTSIKVKVDNAADLSESYF 230

DB 334 EEKFSHFAYVKKPNQSLTSVTVTGQVTSYGKQSA---NNPTVKVYKHIGSDELAESVY 389

QY 231 V--NPENFEDVTNSVNITFPNPQYKVEFNTPDDQITTPYIVVNGHIDPNKSGDLALR 287

DB 390 AKLDPTSKFEDVTEKVNLSYTSNGGYTLNLGLDN--SKDYVIKYEGEYDQNAK-DLNR 446

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

QY 288 STLGYNSNIWR-----SMSWDNEVAFNNGSGSGDIDKPVVP 326

DB 447 THLSGYHKYPPYPPYPPYVQVLTWNNGVAFYSNNAKGDGDKDPNDP 493

R.Nilsson, M.; Frykberg, L.; Flock, J.I.; Pei, L.; Lindberg, M.; Guss, B.
Infect. Immun. 66, 2666-2673, 1998
A/Title: A Fibrinogen-binding protein of Staphylococcus epidermidis.
A/Reference number: Z20781; MUID:98261511; PMID:9596732
A/Accession: T30214
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1092 <NII>
A/Cross-references: EMBL:Y17116; NID:e1296734; PID:e1296735; PIDN:CAA76638.1

Query Match 20.2%; Score 349; DB 2; Length 1092;
Best Local Similarity 30.3%; Pred. No. 6.1e-14;
Matches 100; Conservative 61; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLTNVTGVI-DSGTTVYPHQAGYVKLNYSFVSNSAVKGDTFKIVPKELNLNGVTS 71
Db 287 VTDQ--SITEGYDSEGVKAHAENLIYDVTFEYDVKVSGDTMTVDIDKNTVPSDLTD 344
QY 72 TAKVPRIMAGD-QVLANGVIDS-DGNVIYTFDYVNTKDVKATLTMPAYIDPENVKKTG 129
Db 345 SFTIPKIDNSGEIATGYDKNKQITFTFDYDKYENIKAKLKLTSYIDKSKVPNNN 404
QY 130 ---NVTLATIGSTTANKTVLVDEYKYGKFPYNLSIKGTIDQIDKTNNTYRQTIYVNPSCD 186
Db 405 TKLDVEYKTALSS--VNKTTVEYQRPNENRNLQSMFTNIDTKMHTVBQTIYINPL-- 460
QY 187 NVIAPVLTLGNLKPNNTDSNALIDQNTSIKVKYVDNAADLSESYFV-NPENEDEVTSVNI 245
Db 461 RYSAKETNWNISGNGDEGSTIIDSTIIKVKYGDNQNLPSNRIYDYSEVEDVTNDXYA 520
QY 246 TFPNPNQYKVEFNTPDQITTPYIVVNGHIDPNSKGD-----LALRSTLYGYSNII 298
Db 521 QLGNNNDVNINFG----NIDSPYIIKIVISKYDPN-KDDYTTIQQTVMQTTINEYTG-- 573
QY 299 WRSMWDNEVAFNNGSGSGDGIDKPVPEQ 328
Db 574 FRTASYDNTIAFSTSSGGQG-DLP--PEK 600

RESULT 6
A32192
fibronectin-binding protein - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C/Accession: A32192
R/Signaes, C.; Rautcci, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoecek, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A/Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylococcus aureus.
A/Reference number: A32192; MUID:89098998; PMID:2521391
A/Accession: A32192
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-1018 <SIG>
A/Cross-references: GB:J04151
C/Keywords: fibronectin binding

Query Match 19.1%; Score 331; DB 2; Length 1018;
Best Local Similarity 24.6%; Pred. No. 7.3e-13;
Matches 82; Conservative 77; Mismatches 146; Indels 28; Gaps 11;

QY 10 GTDITNQLTNVTGIDSG---TTVYPHQAGYVKLNYSFVSNSAVKGDTFKIVPKELN 65
Db 194 GTDVTSKVT-VEIGSIEGHNNNTKVEPHAGQRAVLKYLKFENGLHGGDYFDFTLSNNVN 252
QY 66 LNGVTSTAKVPRIMAGDQVLANGVIDSDGNVIYTFDYVNTKDVKATLTMPAYIDPENV 125
Db 253 THGVSTARKVPEIKNGSVMAATGEVLGEGKIRYTFNTDIEDKVDVTALEINLFDPKTV 312
QY 126 KKTGNVTLATGIGSTTANKTVLVYD-EKYGKFPYNLSIKGTIDQIDKTNNTYRQTIYVNP 184
Db 313 QTNNGQITITSTLNEBQTSKELDVKKYKDIGNY-ANLNGSIETFNKANNRFSHVAFIKPN 371
QY 185 GDNVIAFVLTLGNLKPNNTDSNALIDQNTSIKVKY-VDNAADLSESYFVN--PENFEDVT 240

Db 372 NGKTTSVTLTGILMKGSNQNG---NQPKVRLFEYLGNNEDIKSVYANTTDTSKFEKVT 427
QY 241 NSV--NITFPNPNQYKVEFNTPDQITTPYIVVNGHIDPNSKGDIALRSTLYGYSNII 298
Db 428 SNMSGNLNLQNGSYSINI---ENLDKTYVVAHYDGEY-LNGTDEVDFRTQWGHPEOLY 482
QY 299 -----WRSMWDNEVAFNNGSGSGDGIDKPVV 325
Db 483 KYYYDRGYTLTWDNGLVLYSNKANGENKGPIT 515

RESULT 7
H90053
hypothetical protein fnb [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: H90053
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: H90053
A/Status: preliminary.
A/Molecule type: DNA
A/Residues: 1-1038 <KUR>
A/Cross-references: GB:BA00018; PID:g13702453; PIDN:BAB43594.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A/Gene: fnb

Query Match 18.7%; Score 324.5; DB 2; Length 1038;
Best Local Similarity 26.9%; Pred. No. 1.9e-12;
Matches 91; Conservative 68; Mismatches 154; Indels 25; Gaps 11;

QY 10 GTDITNQLTNVTGIDS-GTTVYPHQAGYVKLNYSFVSNSAVKGDTFKIVPKELNLN 67
Db 189 GTDVTSKVTVESGSIAPQGNKVEPHAGQRAVLKYLKFPADGLKRGDYFDFTLSNNVNTY 248
QY 68 GVTSTAKVPRIMAGDQVLANGVIDSDGNVIYTFDYVNTKDVKATLTMPAYIDPENVK 127
Db 249 GVTSTARKVPEIKNGSVMAATGEILGNINIRYTFNTEHKEVEVTANLEINLFDPKTVQS 308
QY 128 TGNVTLATGIGSTTANKTVLVDEYKYGKFPYNLSIKGTIDQIDKTNNTYRQTIYVNPSCDN 187
Db 309 NGEQKITSKLNGEETKTFPVYVNPVSNSTYVNWGSIETFNKESNKFTHIAYIKPMNGN 368
QY 188 VIAPV-LTGNLKPNNTDSNALIDQNTSIKVKY-VDNAADLSESYFVNPN--FEDVTNS 242
Db 369 QSNVTASVTGTL--TEGSNLAGQPT-VKVEYELGKKDELPSQSVYANTSDTNKFDVTK 424
QY 243 VN--ITFPNPNQYKVEFNTPDQITTPYIVVNGHIDPNSKGDIALRSTLYG-----YNS 295
Db 425 MNGKLSYQDNGSYSINL---DKLDKTYVIHYTGEVYLGSD-QQVNFRTETLYGYPBRAYKS 479
QY 296 NIWRS--MSWDNEVAFNNGSGSGDGIDKPVPEQPD 331
Db 480 YYYVGGYRLTWDNGLVLYSNKADGNGKNGQIIQDNDFE 517

RESULT 8
T28680
fibrinogen-binding protein homolog - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
C/Accession: T28680
R/Josefsson, E.; McCrea, K.; Ni Eidhin, D.; O'Connell, D.; Cox, J.; Hook, M.; Foster, T.; Microbiology 144, 3387-3395, 1998
A/Title: Three new members of the serine-aspartate repeat protein multigene family of Staphylococcus aureus.
A/Reference number: Z20510; MUID:99098700; PMID:9884231
A/Accession: T28680

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1166 <JOS>
A;Cross-references: EMBL:AJ005647; NID:e1318793; PID:e1318794; PIDN:CAA06652.1
C;Genetics:
A;Gene: sdre

Query Match 18.7%; Score 323.5; DB 2; Length 1166;
Best Local Similarity 31.2%; Pred. No. 2.6e-12;
Matches 111; Conservative 53; Mismatches 137; Indels 55; Gaps 18;

QY 2 VAADAPAGTDITNQLTNT-----VGIDSGTTVYPHOAGYVKLNNGFSVPNSAVKGDTE 56
DB 269 VAQPAVAASNNV-NDLIKVTIKQTIVGDKDNVAAAHGKDIEYDTEFTIDNKVKKGDTE 327
QY 57 KI-----TVPEKELNNGVTSTAKVPPIMAGD---QVLANGVID-SDGNVITYFTDYVNTK 107
DB 328 TINYDKNVIPSDL-----TDKNDPIDITDPSGEVIAKGFEDKATKQITTYTFTDYVDKY 380
QY 108 DVKATLTMPAYIDPENY--KKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTI 165
DB 381 EDIKSRILTYSIDKKTVPNETSLNLTFAATAGKETSON--VTVDYQDPMVHGDSNIQSIF 438
QY 166 DQDKTNNTYRQTIYVNP---SGDNVIAPVL-----TGNLKPNLSDNALIDQNTSIKV 216
DB 439 TKLDEKQITEQOIYVNPPLKKSATNTKVDIAGSQVDYGNIKLGNGS-TIID-QNTEIKV 496
QY 217 YKVDNADLSESYFV-NPENFEDVTSVNTFPNPQYKVEFNTPD-DQITPYIVVNG 274
DB 497 YKVNSDQQLPQSNRIYDFSQYEDVTSQ---FDNKKSFNNVATLDFGDINSAYIIRKVS 552
QY 275 HIDPNSKGD-----ALRST-LYGYSNIIWRMSMWDEVAFFNNGSGSGDGDIDKP 323
DB 553 KYTPTSDELDIAQGTSMRTDKYGY-----YNYAGYSNFIIVTSNDTGCGDGTVPK 603

RESULT 9

E89824
hypothetical protein sdre [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: E89824
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89824
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1141 <KUR>
A;Cross-references: GB:BA000018; PID:g13700455; PIDN:BAB41752.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: sdre

Query Match 18.5%; Score 320.5; DB 2; Length 1141;
Best Local Similarity 30.4%; Pred. No. 3.8e-12;
Matches 108; Conservative 55; Mismatches 139; Indels 53; Gaps 17;

QY 2 VAADAPAGTDITNQLT---NTVGDISGTTVYPHOAGYVKLNNGFSVPNSAVKGDTEFX 57
DB 264 VAQPAVAASNNVNDLITVTKQTIKVGDKDNVAAAHGKDIEYDTEFTIDNKVKKGDTEMT 323
QY 58 I-----TVPEKELNNGVTSTAKVPPIMAGD---QVLANGVID-SDGNVITYFTDYVNTKD 108
DB 324 INYDKNVIPSDL-----TDKNDPIDITDPSGEVIAKGFEDKATKQITTYTFTDYVDKYE 376
QY 109 DVKATLTMPAYIDPENY--KKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTID 166
DB 377 DIKARLTLYSYIDKQAVPNETSINLTFAATAGKETSON--VSVDYQDPMVHGDSNIQSIFT 434

QY 167 QIDKTNNTYRQTIYVNP---SGDNVIAPVL-----TGNLKPNLSDNALIDQNTSIKVY 217
DB 435 KLDEKQITEEQIYVNPPLKKTATNTKVDIAGSQVDYGNIKLGNGS-TIID-QNTEIKVY 492
QY 218 KVDNADLSESYFV-NPENFEDVTSVNTFPNPQYKVEFNTPD-DQITPYIVVNGH 275
DB 493 KVPNQQLPQSNRIYDFSQYEDVTSQ---FDNKKSFNNVATLDFGDINSAYIIRKVS 548
QY 276 IDPNSKGD-----ALRST-LYGYSNIIWRMSMWDEVAFFNNGSGSGDGDIDKP 323
DB 549 YTPTSDELDIAQGTSMRTDKYGY-----YNYAGYSNFIIVTSNDTGCGDGTVPK 598

RESULT 10

F90070
Clumping factor B [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F90070
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F90070
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-877 <KUR>
A;Cross-references: GB:BA000018; PID:g13702588; PIDN:BAB43728.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: clfb

Query Match 18.0%; Score 312.5; DB 2; Length 877;
Best Local Similarity 24.9%; Pred. No. 8.4e-12;
Matches 92; Conservative 69; Mismatches 132; Indels 77; Gaps 15;

QY 6 APAAGTDITNQLTNTVTVGIDSGTTVYPHOAGYVKLNNGFSVPNSAVKGDTEFKITVPKELN 65
DB 208 ADAKGTNVNDKVTASNFKLEK-TTPDENQSGNTFMAANFTVTDKVSQDYF----- 257
QY 66 LNVGTSTAKVPPIMAGDQVLANGVID-----SDGNVI----- 97
DB 258 -----TAKLP-----DSLGTNGDVVYSNSNNTMPIADIKSTNGDVVAKATYDILTKTYT 306
QY 98 YFTFDYVNTKQDVKATLTMPAYIDPENYKKTGNVTLATGIGSTTANKTVLVDEYK---Y 153
DB 307 FVFTDYVNNKENINGQFSLPLFTDRAKAPKSGTYDANINIADEMENNKITTYNYSPIAGI 366
QY 154 GKFNLSIKGTIDQIDKTN--NTYRQTIYVNP---GDNVIAVLTGNLKPNTDSNALI 207
DB 367 DKPNGANISSQILIGVDLTASGQNTYKQIVFVNPQKQVLGNTWV--YIKGYQDKIESSGKY 424
QY 208 DQQNTSIKVKVNDNAADLSESYFVNP--ENFEDVTSV--NITPENPQYKVEFNTPPDQ 263
DB 425 SATDTKLRIFEVNDTSKLSDSYADPNDNLKEVTDQFKNRIYEHFNVAISIKFG---D 480
QY 264 ITTPYIVVNGHIDPNSKGDALRSTLYGYN---SNIIWRMSMWDEVAFFNNGSGSGDG 319
DB 481 ITKTYVVLVEGHYDNTGKN--LKTQVIGENVDPVTNRDYSIFGMNENNVVRYGGGSADG 537
QY 320 IDKPVPEQP 329
DB 538 -DSAVNPKDP 546

RESULT 11

T28679
fibrinogen-binding protein homolog - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
C;Accession: T28679

R;Josefsson, E.; McCrea, K.; Ni Eidhin, D.; O'Connell, D.; Cox, J.; Hook, M.; Foster, T.
Microbiology 144, 3387-3395, 1998
A;Title: Three new members of the serine-aspartate repeat protein multigene family of St
A;Reference number: Z20510; MUID:99098700; PMID:9884231
A;Accession: T28679
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1315 <JOS>
A;Cross-references: EMBL:AJ005646; NID:e1318791; PID:e1318792; PIDN:CAA06651.1
C;Genetics:
A;Gene: sdrD

Query Match 14.9%; Score 257.5; DB 2; Length 1315;
Best Local Similarity 26.9%; Pred.No.3.8e-08;
Matches 88; Conservative 51; Mismatches 157; Indels 31; Gaps 12;

QY 13 ITNQLTNVTGIDSGTIVYPHQAGYVKLNFGFSVPNSAVKGDTFKITVPEKELNLNGVT-- 70
DB 251 ITSNTTLTVVDADKNNKIIVPAQ-DYLSLKSQITVDDKVKSGDYFTIKYSDTVQVYGLNPE 309
QY 71 -----STAKVPPIMAGDQVLANGVIDSDGNVI-YTFTDYVNTKDDVKATLTMPAYIDPEN 124
DB 310 DIKNIGDIKP--NNGETIATAKHDTANNLITYTFTDYVDRNSVQMGINYSIYMDADT 366
QY 125 VKRTGN-VTLATGIGSTTANKTVLVLDYEKYGKFNLSIKG---TIDQIDKTNT--YRQ 177
DB 367 IPVSKNDVEFNVLTIGNTTTKTANIQPYDVVNEKNSIGSAFTETVSHVGNKENPGYKQ 426
QY 178 TIYVPSGDNVIAVPLTGNLKPNNTDSNAL-IDQNTSIKVKVDNAADLSESYFVNPN 235
DB 427 TIYVPSSENSLTNAKLKVQAHSSYPNNIGQINKDVTIDIKIYQVPKGYTLNKGVDNTKE 486
QY 236 FEDVTVNSV--NITFPNPQYKVEFNTPDQITTPYIVVNGHID-PNSKGLALRSTLYG 292
DB 487 LIDVTNQYLQKITYGDNNSAVIDFGNAD---SAYVVMWNTKFQYTNSESPTLVQMATLS 542
QY 293 YNSNIWRSMWSDNEVAFNNGSGSDG 319
DB 543 STGN---KSVSTGNALGFTNNQSGAG 566

RESULT 12

hypothetical protein sdrD [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: D89824
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89824
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1385 <KUR>
A;Cross-references: GB:BA000018; PID:g13700454; PIDN:BAB41751.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: sdrD

Query Match 13.9%; Score 240.5; DB 2; Length 1385;
Best Local Similarity 26.1%; Pred.No.4.7e-07;
Matches 86; Conservative 54; Mismatches 154; Indels 35; Gaps 14;

QY 13 ITNQLTNVTGIDSGTIVYPHQAGYVKLNFGFSVPNSAVKGDTFKITVPEKELNLNGVT-- 70
DB 251 ITSNTTLTVVDADNSKTIIVPAQ-DYLSLKSQITVDDKVKSGDYFTIKYSDTVQVYGLNPE 309
QY 71 -----STAKVPPIMAGDQVLANGVIDSDGNVI-YTFTDYVNTKDDVKATLTMPAYIDPEN 124
DB 310 DIKNIGDIKP--NNGETIATAKHDTANNLITYTFTDYVDRNSVKMGINYSIYMDADT 366

QY 125 V---KKTGNVTLATGIGSTTANKTVLVLDYEKYGKFNLSIKG---TIDQIDKTNT--Y 175
DB 367 IPVDKK--DVPFSVTIGNQITTTADITPYAKEADNNSIGSAFTETVSHGVNVEDPGY 424
QY 176 RQTIYVPSGDNVI-APVLTGNLKPNNTDSN-ALIDQNTSIKVKVDNAADLSESYFVNP 233
DB 425 NQVYVNPMDKDLKGAKLVEAYHPKYPNTIGNQINQNTNIKIRVPEGYTLNKGVDNT 484
QY 234 ENFEDVTVNSV--NITFPNPQYKVEFNTPDQITTPYIVVNGHID-PNSKGLALRSTL 290
DB 485 NDLDVDTDEFKKNKMTYGSNSVNLDFG---DITSAYVMWNTKFQYTNSESPTLVQMAT 540
QY 291 YGYNSTIWRSMWSDNEVAFNNGSGSDG 319
DB 541 LSSTGN---KSVSTGNALGFTNNQSGAG 566

RESULT 13

hypothetical protein sdrC [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: C89824
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89824
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-953 <KUR>
A;Cross-references: GB:BA000018; PID:g13700453; PIDN:BAB41750.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: sdrC

Query Match 13.3%; Score 229.5; DB 2; Length 953;
Best Local Similarity 24.9%; Pred.No.1.4e-06;
Matches 84; Conservative 56; Mismatches 157; Indels 41; Gaps 12;

QY 6 APAAGTIDITNQL--TNVTVGIDSG-----TTVYPHQAGYVKLNFGFSVPNSAVKGD 55
DB 178 APQGTIVNDKVHFTNIDIALDKGHVNTGTNTEFMATSSDVLKLKANTTIDDSYKSGDT 237
QY 56 FKITVPEKELNLNGVTSTAKVPPIM-AGDQVLANGVIDSDGN-VITFTDYVNTKDYKAT 113
DB 238 FTFKYGQYFRPGSVRLPSQQLNLYNAQNIIAKGIYDSKTNTTFTFTYVVDQYTVNVS 297
QY 114 LTMPAYIDPEN--VKKTG--NVTLATGIGSTTANKTVLVLDYEKYGKFNLSIKGTTDQI 168
DB 298 FEQVAFARENATTDKTAIYKMEVTL---GNDTYSKDYAVLDYGNQKGQQLISSTNYINNE 353
QY 169 DKTNTNYRQTIYVPSGDNVIAVPLTGNL--KPNDSNALIDQNTSIKVKVDNAADL 225
DB 354 DLSRN--MTVYNQPKKTYTKETFTVNLTGKFNPDAR-----NFKIYEVTDONOF 402
QY 226 SESYFVNPNFEDVTVNSVNTFPNPQ--YKVEFNTPDQITTPYIVVNGHIDPNSKGL 284
DB 403 VDSFTPTDSKLKDVLTGQFDVIYSDNKTATVDLLNGQSSDGQYIIQVAYPDNSITDNG 462
QY 285 ALRSTLYGNSNIWRSMWSDNEVAFNNGSGSDGIDK 322
DB 463 KIDYTLLETONG----KSSWSNSYSNVNGSSTANGDQK 495

RESULT 14

protein F2 - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000

C/Accession: T30856
R/Jaffe, J.; Natanson-Yaron, S.; Caparon, M.G.; Hanski, E.
Mol. Microbiol. 21, 373-384, 1996
A/Title: Protein F2, a novel fibronectin-binding protein from *Streptococcus pyogenes*, pp
A/Reference number: Z20907; MUID:97011581; PMID:8858591
A/Accession: T30856
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-1039 <JAF>
A/Cross-references: EMBL:U31980; NID:g1654115; PID:g1654116; PIDN:AAC44522.1
C/Genetics:
A/Note: PRTF2

Query Match	10.5%;	Score 182;	DB 2;	Length 1039;
Best Local Similarity	21.9%;	Pred. No. 0.0014;		
Matches	81;	Conservative	78;	Mismatches 149;
			Indels	62;
			Gaps	18;

[illegible]

RESULT 15

AG1542

wall associated protein precursor (LPXTG motif) homolog lin0879 [imported] - *Listeria in*
 C;Species: *Listeria innocua*

C;Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text_change 27-Nov-2001

C;Accession: AG1542

R; Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

A;Title: Comparative genomics of *Listeria* species.
OK, C.; Schneider, I.; Simoes, N.; Ierliez, A.; Vazquez-Borana, O.A.; Voss, M.; Hendrickson

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AG1542

A;Status: preliminary

A;molecule type: DNA

A;Residues: 1-463 <GLA>

A: Experimental source: strain Clp11262

A;Gene: lin0879

Query Match	9.3%;	Score 161.5;	DB 2;	Length 463;
Best Local Similarity	24.9%;	Pred. No. 0.0086;		
Matches	88;	Conservative	48;	Mismatches 129;
			Indels	89;
			Gaps	18;

```

QY      9 .AGTDI -TNQLTNTVTGIDSGTTVP-P-HQAGYVKLNFGFSVPNSAVKGDTEKITVPKEJNL 66
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db      25 AATDYGSSFEFTNVALQNQNGDPVTNFKENSKVRVAYDFVITQPVVSGETIMTLTITPDQLKL 84
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
QY      67 NGVTSTAKVPPIMAGDQVLANGVID-SDGNVIYTFTDYVNTKDVAKILTMPAYIDPENV 125
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db      85 ---INFGFVPNDASGNTIANATIDPATGTTITLTFTHYVNTHTNLGSLFYNAIFNSKNI 141
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
QY      126 KK-----TGNVTLATIGISTANKTVLVDYEKYKGFYNLSIKGTI 165
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db      142 QTDQVNPFIQFPVNTTQTINTIYISKVTTGGGTGSPTI-----VFKQGRM 185
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
QY      166 DQIDKTNTTYRQTIYVNPSPGDNVIAP---VLGNLKPNTDSNALIDQNTSIKVKYVDN 221
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db      186 D-DKDTSLIHWTVTLN---NALTPIDNAIYTDTL--GTGQNLTL--GNATIK-YRDAN 233
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
QY      222 AADLSESYFVNP-----ENFEDVTNSVNTFPPNPNOYKVEFNTPPDQITTPYIVVNGH 275
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db      234 KKVLTSTN-VQPIALDSNRNFELTIGTLN-----NQSVV--ITYDTKITTKQKSYTN-- 281
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
QY      276 IDPNSKGDALRSTLYGYNSNIIWRSM$WDNEVAFNNGSGSGDGIKDPVYEOP 329
      | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db      282 -----KATLSGDNLDVAVSRNATVND--YSGSGQGTGTPPPTPPEYKEEP 322

```

Search completed: March 26, 2004, 05:08:54
Job time : 38.039 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:50:40 ; Search time 125.592 Seconds
(without alignments)
744.658 Million cell updates/sec

Title: US-10-056-052A-4
Perfect score: 1732
Sequence: 1 MVAADAPAGTDTITNQLTNV.....NGSGSGDIDKPVVEQPD E 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1732	100.0	331	5	AAE29263 Staphyloc
2	1732	100.0	345	2	AAW31555 Firdonect
3	1727	99.7	520	5	AAE29262 Staphyloc
4	1727	99.7	933	3	AAV58435 Staphyloc
5	1727	99.7	933	4	AAB69508 Staphyloc
6	1727	99.7	933	6	ABJ18947 Pathogen
7	1723	99.5	927	6	ABM72221 Staphyloc
8	1723	99.5	936	2	AAW89801 Staphyloc
9	1518	87.6	1021	4	AAU33975 Staphyloc
10	1518	87.6	1021	4	AAU36951 Staphyloc
11	1517	87.6	935	6	ABU16402 Protein e
12	1433	82.7	496	5	AAU75490 S. aureus
13	1433	82.7	496	6	ADA89664 Staphyloc
14	1433	82.7	496	6	ADA89663 Staphyloc
15	416.5	24.0	961	6	ABU15854 Protein e
16	409	23.6	767	4	AAU34403 Staphyloc
17	409	23.6	767	4	AAU37547 Staphyloc
18	409	23.6	940	2	AAU37070 Fibronect
19	409	23.6	940	6	ABU19111 Pathogen
20	409	23.6	948	6	ADA89470 Staphyloc
21	409	23.6	948	6	ABU18923 Pathogen
22	409	23.6	948	6	ABM72536 Staphyloc
23	353	20.4	343	7	ABM79016 Staphyloc
24	353	20.4	560	7	ABM79015 Staphyloc
25	353	20.4	892	6	ABU42557 Protein e

26	353	20.4	930	5	ABP40469 Staphyloc
27	353	20.4	991	3	AAY83171 Cell wall
28	353	20.4	991	3	AAY70120 Staph. ep
29	349	20.2	549	7	ABM79020 Staphyloc
30	349	20.2	1092	2	AAW41602 Staphyloc
31	349	20.2	1092	7	ABM79019 Staphyloc
32	346	20.0	978	4	AAU33960 Staphyloc
33	346	20.0	1001	4	AAU37093 Staphyloc
34	339	19.6	1018	4	AAU37245 Staphyloc
35	339	19.6	1018	4	AAU34301 Staphyloc
36	339	19.6	1018	6	ABU18922 Pathogen
37	331	19.1	1018	1	AAU37093 Staphyloc
38	331	19.1	1018	6	ABM72537 Fibronect
39	331	19.1	1027	2	AAW89806 Staphyloc
40	324.5	18.7	1038	6	ABU15903 Protein e
41	323.5	18.7	1166	2	AAU08643 S. aureus
42	323.5	18.7	1166	6	ABU18982 Pathogen
43	320.5	18.5	1141	6	ABU42327 Protein e
44	312.5	18.0	567	6	ADA89555 Staphyloc
45	312.5	18.0	743	6	ADA89690 Staphyloc

ALIGNMENTS

RESULT 1					
ID	AAE29263	standard; protein; 331 AA.			
XX	AAE29263;				
AC					
XX					
DT	27-JAN-2003	(first entry)			
XX					
DE	Staphylococcus aureus Clf33 protein.				
XX					
KW	Clumping factor A; ClfA; fibrinogen; fibrin; Clf33; Clf33; N3 protein;				
KW	immunological; staphylococcal infection; impetigo; pneumonia; furuncle;				
KW	septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.				
XX					
OS	Staphylococcus aureus.				
XX					
PN	WO200272600-A2.				
XX					
PD	19-SEP-2002.				
XX					
PF	28-JAN-2002; 2002WO-US002296.				
XX					
PR	26-JAN-2001; 2001US-0264072P.				
PR	12-MAR-2001; 2001US-0274611P.				
PR	18-JUN-2001; 2001US-0298413P.				
PR	30-JUL-2001; 2001US-0308116P.				
XX					
PA	(INH1-) INHIBITEX INC.				
XX					
PI	Patel JM, Hutchins JT, Domanski P, Patel P, Hall A;				
XX					
DR	WPI; 2002-759834/82.				
DR	N-PSDB; AAD46862.				
XX					
PT	New anti-clumping factor A (ClfA) monoclonal antibody, useful for				
PT	treating or preventing Staphylococcus aureus infection e.g. wound				
PT	infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in				
PT	a human or animal.				
XX					
PS	Claim 9; Page 70-72; 80pp; English.				
XX					
CC	The invention relates to monoclonal antibody which binds the clumping				
CC	factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA				
CC	monoclonal antibody is useful for treating or preventing S. aureus				
CC	infection in a human or animal, and for inhibiting the binding of				
CC	staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment				
CC	S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3				
CC	protein is useful for inducing an immunological response in a human or				
CC					

CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus Clf33 protein
XX

SO Sequence 331 AA;

Query Match 100.0%; Score 1732; DB 5; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.2e-116;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAADAPAGTDITNQLTNVTYVGIDSGTIVPHQAGYKLNNGFSVPNSAVKGDTEKITV 60
DB 1 MVAADAPAGTDITNQLTNVTYVGIDSGTIVPHQAGYKLNNGFSVPNSAVKGDTEKITV 60
QY 61 PKELNNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYFTFDYVNTKDDVKATLTMPAYI 120
DB 61 PKELNNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYFTFDYVNTKDDVKATLTMPAYI 120
QY 121 DPENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQITIY 180
DB 121 DPENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQITIY 180
QY 181 VNPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYVDNAADLSESYFVNPNEDYV 240
DB 181 VNPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYVDNAADLSESYFVNPNEDYV 240
QY 241 NSVNITFPNPQYKVEFNTPPDQITTPYIVVNGHIDPNSKGDALRSTLYGNSNIITWR 300
DB 241 NSVNITFPNPQYKVEFNTPPDQITTPYIVVNGHIDPNSKGDALRSTLYGNSNIITWR 300
QY 301 SMSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 331
DB 301 SMSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 331

RESULT 2
AAW31555
ID AAW31555 standard; protein; 345 AA.

XX AAW31555;
AC AAW31555;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
DE Fibronectin-binding MSCRAMM derivative PCF33.
XX
KW Fibronectin; PCF33; collagen binding protein; sepsis; infection;
KW microbial surface component regonising adhesive molecule; MSCRAMM;
KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
OS Staphylococcus aureus.

FH Key Location/Qualifiers
FT Peptide 1.12
FT /note= "vector pQE30-derived peptide"

XX WO9743314-A2.

XX PD 20-NOV-1997.

XX PF 14-MAY-1997; 97WO-US008210.

XX PR 16-MAY-1996; 96US-0017678P.

XX PA (TEXA) UNITV TEXAS A & M SYSTEM.

XX PA (UABR-) UAB RES FOUND.

XX PI Hoecek M, Patti JM, House-Pompeo K, Schanam N, Symersky J;

XX DR WPI; 1998-008801/01.

XX PT Antibody that interacts with collagen binding domain of Staphylococcal

PT cna gene product - useful to prevent bacterial sepsis in animal infected
XX with Staphylococcus aureus.

PS Disclosure; Page 91; 143pp; English.

XX
CC This protein comprises Staphylococcus aureus fibronectin-binding
CC microbial surface component regonising adhesive matrix molecule (MSCRAMM)
CC derivative PCF33, plus a vector-derived N-terminal peptide. The invention
CC relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
CC aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
CC AAW31552-54) that confer protection against S. aureus infection. CBP
CC protein and antigenic epitopes are contemplated for use in the treatment
CC of pathological infections, especially to prevent bacterial adhesion to
CC collagen. The epitopes are also contemplated for use in the preparation
CC of vaccines and as carrier proteins in vaccine formulations, as well as
CC in the formulation of compositions for the prevention of S. aureus
CC infection. PCF33 and PQD (see AAW31556) were used to raise anti-MSCRAMM
CC polyclonal antibodies used in passive immunisation against bovine
CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (updated on 27-
CC AUG-2003 to correct OS field.)
XX

SO Sequence 345 AA;

Query Match 100.0%; Score 1732; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.4e-116;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAADAPAGTDITNQLTNVTYVGIDSGTIVPHQAGYKLNNGFSVPNSAVKGDTEKITV 60
DB 13 MVAADAPAGTDITNQLTNVTYVGIDSGTIVPHQAGYKLNNGFSVPNSAVKGDTEKITV 72
QY 61 PKELNNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYFTFDYVNTKDDVKATLTMPAYI 120
DB 73 PKELNNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYFTFDYVNTKDDVKATLTMPAYI 132
QY 121 DPENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQITIY 180
DB 133 DPENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQITIY 192
QY 181 VNPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYVDNAADLSESYFVNPNEDYV 240
DB 193 VNPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYVDNAADLSESYFVNPNEDYV 252
QY 241 NSVNITFPNPQYKVEFNTPPDQITTPYIVVNGHIDPNSKGDALRSTLYGNSNIITWR 300
DB 253 NSVNITFPNPQYKVEFNTPPDQITTPYIVVNGHIDPNSKGDALRSTLYGNSNIITWR 312
QY 301 SMSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 331
DB 313 SMSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 343

RESULT 3

AAE29262
ID AAE29262 standard; protein; 520 AA.

XX AAE29262;

XX DT 27-JAN-2003 (first entry)

XX DE Staphylococcus aureus Clf40 protein.

XX
KW Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX

XX OS Staphylococcus aureus.

XX PN WO200272600-A2.

XX PD 19-SEP-2002.

XX PF 28-JAN-2002; 2002WO-US002296.

XX 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
XX 18-JUN-2001; 2001US-0298413P.
PR 30-JUL-2001; 2001US-0308116P.
XX
PA (INH1-) INHIBITEX INC.
XX
PI Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
DR WPI: 2002-759834/82.
DR N-PSDB; AAD46861.
XX
PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
PT a human or animal.
XX
PS Claim 9; Page 67-69; 80pp; English.
XX
CC The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus Clf40 protein
XX
SQ Sequence 520 AA;
XX
Query Match 99.7%; Score 1727; DB 5; Length 520;
Best Local Similarity 100.0%; Pred. No. 9.2e-116;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAADAPAPAGTDITNQLTNVTNVGIDSGTTVYPHQAGYVKLNFGFSVPNSAVKGDTEKITVP 61
Db 182 VAADAPAPAGTDITNQLTNVTNVGIDSGTTVYPHQAGYVKLNFGFSVPNSAVKGDTEKITVP 241
QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLTMPAYID 121
Db 242 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLTMPAYID 301
QY 122 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFPYNLSIKGTIDQIDKTNNTYRQTIYV 181
Db 302 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFPYNLSIKGTIDQIDKTNNTYRQTIYV 361
QY 182 NPSGDNVIAFVLTLGNLKPNLSDNALIDQNTSISKYKYVDNAADLSESYFVNPENFEDVTN 241
Db 362 NPSGDNVIAFVLTLGNLKPNLSDNALIDQNTSISKYKYVDNAADLSESYFVNPENFEDVTN 421
QY 242 SVNITFPNPQYKVEFNTPDDQITTPYIVVNGHIDPNSKGDLLRSTLYGNSNIIRWS 301
Db 422 SVNITFPNPQYKVEFNTPDDQITTPYIVVNGHIDPNSKGDLLRSTLYGNSNIIRWS 481
QY 302 MSWDNEVAFNNGSGSGDGIDKRVYVEQPD 331
Db 482 MSWDNEVAFNNGSGSGDGIDKRVYVEQPD 511
XX
RESULT 4
ID AAY58435 standard; protein; 933 AA.
XX
AC AAY58435;
XX
DT 27-MAR-2000 (first entry)
XX
DE Staphylococcus aureus fibrinogen binding ClfA protein.
XX
KW ClfA; fibrinogen binding protein; bacterial colonisation;

KW indwelling medical device; staphylococcal infection.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Reptide 1..39
FT /note= "Signal peptide"
FT Region 40..559
FT /note= "Region A"
FT Region 332..550
FT /note= "fibrinogen-binding region"
FT Region 560..867
FT /note= "Region R"
FT Region 896..900
FT /note= "Gram positive wall-associated consensus motif"
XX
PN US6008341-A.
XX
PD 28-DEC-1999.
XX
PF 22-AUG-1994; 94US-00293728.
XX
PR 22-AUG-1994; 94US-00293728.
XX
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
XX
PI Foster TJ, Mcdevitt DL;
XX
DR WPI: 2000-096389/08.
DR N-PSDB; AA255832.
XX
PT Nucleic acid encoding the fibrinogen-binding protein of Staphylococcus
PT aureus, useful for treatment or prevention of infections.
XX
PS Disclosure; Fig 2A-1-4; 35pp; English.
XX
CC This sequence represents the Staphylococcus aureus fibrinogen-binding
CC protein, ClfA. ClfA is an important receptor involved in S. aureus
CC colonisation of indwelling medical devices (e.g., catheters, artificial
CC heart valves). Shortly after implantation, the surfaces of medical
CC devices become coated with host plasma and matrix proteins such as
CC fibrinogen and fibronectin, and there is considerable evidence to suggest
CC that bacterial adherence to fibrinogen/fibrin is important in the
CC initiation of device-related infection. The fibrinogen-binding region of
CC ClfA is thought to reside between residues 332 and 550 in a region
CC designated A. The protein also contains a repeated region (region R)
CC comprising 154 repeats of the dipeptide Ser-Asp, and the C-terminus
CC contains features present in surface proteins of other Gram positive
CC bacteria that are responsible for anchoring the protein to the cell wall
CC and cell membrane. ClfA, or its fragments, may be used to block S. aureus
CC colonisation of wounds, to prevent adherence of S. aureus to indwelling
CC medical devices, as vaccines to protect against S. aureus infection
CC (e.g., mastitis in ruminants), to raise specific antibodies, and for
CC diagnosis (by agglutination or immunoassay). The specific antibodies are
CC used for passive immunisation, to block infection of wounds or adhesion
CC of S. aureus and for diagnosis. Nucleotides encoding ClfA and its
CC fragments may be used as diagnostic probes
XX
SQ Sequence 933 AA;
XX
Query Match 99.7%; Score 1727; DB 3; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAADAPAPAGTDITNQLTNVTNVGIDSGTTVYPHQAGYVKLNFGFSVPNSAVKGDTEKITVP 61
Db 221 VAADAPAPAGTDITNQLTNVTNVGIDSGTTVYPHQAGYVKLNFGFSVPNSAVKGDTEKITVP 280
QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLTMPAYID 121
Db 281 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVITFTDYVNTKDVKATLTMPAYID 340
QY 122 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFPYNLSIKGTIDQIDKTNNTYRQTIYV 181

|||||
Db 341 PENYKKTGNVTLATGIGSTTANKTVLVDYEKYGKFFYNLSIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAFVLGTGNLKPNNTDSNALIDQONTSIKVKYKVDNAADLSESYFVNPFNEDVTN 241
Db 401 NPSGDNVIAFVLGTGNLKPNNTDSNALIDQONTSIKVKYKVDNAADLSESYFVNPFNEDVTN 460
QY 242 SVNITFPNPNQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDLLALRSTLYGYSNIIWRS 301
Db 461 SVNITFPNPNQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDLLALRSTLYGYSNIIWRS 520
QY 302 MSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 331
Db 521 MSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 550

RESULT 5
AAB69508
ID AAB69508 standard; protein; 933 AA.

AC AAB69508;

DT 23-APR-2001 (first entry)

DE Staphylococcus aureus Clfa protein.

KM Staphylococcus aureus; clfa; antibiotic; vaccine;
KW fibrinogen binding protein; bacterial infection; mastitis.

OS Staphylococcus aureus.

PN US6177084-B1.

PD 23-JAN-2001.

PF 19-OCT-1999; 99US-00421868.

PR 22-AUG-1994; 94US-00293728.

PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.

PI Foster TJ, Mcdevitt DL;

DR WPI; 2001-181608/18.

DR N-PSDB; AAF58593.

PT Novel Staphylococcus aureus fibrinogen binding protein useful as vaccine
PT to prevent infection, promote wound healing, block adherence to
PT indwelling medical devices and for diagnosing staphylococcus aureus
infection.

PS Claim 5; Fig 2; 30pp; English.

CC The present sequence is a novel Staphylococcus aureus fibrinogen binding
CC protein. It is useful as a vaccine to protect against human and animal
CC infections caused by S.aureus, such as against mastitis, to block
CC S.aureus from colonising and infecting a wound, to block adherence of
CC S.aureus to indwelling medical devices such as catheters, replacement
CC heart valves and cardiac assist devices. The protein can be used to
CC diagnose bacterial infections. Polyclonal and monoclonal antibodies
CC raised against the fibrinogen binding protein are useful for passively
CC immunising against infections caused by S.aureus, to prevent infection of
CC a wound and to diagnose bacterial infections

XX Sequence 933 AA;

Query Match 99.7%; Score 1727; DB 4; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNLTNTVTGIDSGTTVPYHQAGYVKLNYGFSVPNSAVKGDTEKITVP 61
Db 221 VAADAPAGTDTITNLTNTVTGIDSGTTVPYHQAGYVKLNYGFSVPNSAVKGDTEKITVP 280

QY 62 KELNLNGVTSTAKVPPIMAGDOVLANGVIDSDGNVIYFTDYVNTKDDVKATLTMPAYID 121
Db 281 KELNLNGVTSTAKVPPIMAGDOVLANGVIDSDGNVIYFTDYVNTKDDVKATLTMPAYID 340
QY 122 PENVKKTGNVTLATGIGSTTANKTVLVDYEKYGKFFYNLSIKGTIDQIDKTNNTYRQTIYV 181
Db 341 PENVKKTGNVTLATGIGSTTANKTVLVDYEKYGKFFYNLSIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAFVLGTGNLKPNNTDSNALIDQONTSIKVKYKVDNAADLSESYFVNPFNEDVTN 241
Db 401 NPSGDNVIAFVLGTGNLKPNNTDSNALIDQONTSIKVKYKVDNAADLSESYFVNPFNEDVTN 460
QY 242 SVNITFPNPNQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDLLALRSTLYGYSNIIWRS 301
Db 461 SVNITFPNPNQYKVEFNTPPDDQITTPYIVVNGHIDPNSKGDLLALRSTLYGYSNIIWRS 520
QY 302 MSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 331
Db 521 MSWDNEVAFNNGSGSGDGIDKPVVPEQPDE 550

RESULT 6
ABJ18947
ID ABJ18947 standard; protein; 933 AA.

AC ABJ18947;

DT 06-MAR-2003 (first entry)

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 93.

KW Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KW autoimmune disease; HIV; hepatitis.

OS Staphylococcus sp.

PN WO200259148-A2.

PD 01-AUG-2002.

PF 21-JAN-2002; 2002WO-EP000546.

PR 26-JAN-2001; 2001AT-00000130.

PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

PI Weinke A, Nagy E, Von Ahsen U, Klade C, Henics T, Zauner W;
PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichart T, Hafner M;
PI Tempelmaier B;

DR WPI; 2003-075410/07.

PT Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.

PS Example 7; Page 160; 252pp; English.

CC The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against S. aureus or S. epidermidis. The

CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against S. aureus or S. epidermidis. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
SQ Sequence 933 AA;

Query Match 99.7%; Score 1727; DB 6; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNQLTNVTGIDSGTTYYPHQAGYVKLNFGSVNSAVKGDTEFKITVP 61
DB 221 VAADAPAGTDTITNQLTNVTGIDSGTTYYPHQAGYVKLNFGSVNSAVKGDTEFKITVP 280
QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFDYYNTKDDVKATLTMPAYID 121
DB 281 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFDYYNTKDDVKATLTMPAYID 340
QY 122 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFYNLSIKGTIDQIDKTNNTYRQTIYV 181
DB 341 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFYNLSIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYKVDNAADLSESYFVNPNFEDVTN 241
DB 401 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYKVDNAADLSESYFVNPNFEDVTN 460
QY 242 SVNITFPNPNOYKVEFNTPPDDQITTPYIVVYNGHIDPNSKGDALRSTLYGYSNIIWRS 301
DB 461 SVNITFPNPNOYKVEFNTPPDDQITTPYIVVYNGHIDPNSKGDALRSTLYGYSNIIWRS 520
QY 302 MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 331
DB 521 MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 550

RESULT 7
ABM722221
ID ABM72221 standard; protein; 927 AA.
XX
AC ABM72221;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus protein #1461.
XX
KM Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KM enzymatic assay; antibiotic target.
XX
OS Staphylococcus aureus.
XX
PN WO200294868-A2.
XX
PD 28-NOV-2002.
XX
PF 27-MAR-2002; 2002WO-IB002637.
XX
PR 27-MAR-2001; 2001GB-00007661.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Masignani V, Mora M, Scarselli M;
XX
DR WPI; 2003-120786/11.
DR N-PSDB; ACF73781.
XX
PT New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.

XX
PS Claim 1; SEQ ID NO 2922; 49pp; English.
XX
CC The invention relates to novel genes and encoded proteins from.
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus proteins of the invention
XX
SQ Sequence 927 AA;

Query Match 99.5%; Score 1723; DB 6; Length 927;
Best Local Similarity 99.7%; Pred. No. 3.7e-115;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNQLTNVTGIDSGTTYYPHQAGYVKLNFGSVNSAVKGDTEFKITVP 61
DB 221 VAADAPAGTDTITNQLTNVTGIDSGTTYYPHQAGYVKLNFGSVNSAVKGDTEFKITVP 280
QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFDYYNTKDDVKATLTMPAYID 121
DB 281 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFDYYNTKDDVKATLTMPAYID 340
QY 122 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFYNLSIKGTIDQIDKTNNTYRQTIYV 181
DB 341 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFYNLSIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYKVDNAADLSESYFVNPNFEDVTN 241
DB 401 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYKVDNAADLSESYFVNPNFEDVTN 460
QY 242 SVNITFPNPNOYKVEFNTPPDDQITTPYIVVYNGHIDPNSKGDALRSTLYGYSNIIWRS 301
DB 461 SVNITFPNPNOYKVEFNTPPDDQITTPYIVVYNGHIDPNSKGDALRSTLYGYSNIIWRS 520
QY 302 MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 331
DB 521 MSWDNEVAFNNGSGSGDGIDKPVVPEQPD 550

RESULT 8
AAW89801
ID AAW89801 standard; protein; 936 AA.
XX
AC AAW89801;
XX
DT 16-MAR-1999 (first entry)
XX
DE Staphylococcus aureus protein SEQ ID #5249.
XX
KM Computer readable medium; vaccine; S. aureus infection; immunodetection;
KM cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KM skin infection; surgical wound infection; scalded skin syndrome;
KM toxic shock syndrome.
XX
OS Staphylococcus aureus.
XX
PN EP786519-A2.
XX
PD 30-JUL-1997.
XX
PF 07-JAN-1997; 97EP-00100117.
XX
PR 05-JAN-1996; 96US-0009861P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Kunsch CA, Chol GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;

XX WPI; 1997-374922/35.
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of anti-
PT S.aureus vaccines.
XX Claim 23; Page 3255-3258; 3271pp; English.
XX This sequence represents a Staphylococcus aureus protein sequence of the
CC invention. The DNA sequences encoding the S.aureus proteins are recorded
CC on a computer readable medium, preferably selected from a floppy or hard
CC disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.
CC Homology searches using the S.aureus DNA sequences allows putative
CC functions to be assigned so that protein-encoding or regulatory regions
CC of commercial, therapeutic or industrial importance can be obtained.
CC Specifically, sequences which are likely to encode antigens have been
CC identified and these polypeptides can be used in a vaccine composition
CC against S.aureus infection. The polypeptides can also be used in a kit
CC for the immunodetection of S.aureus in a sample. S.aureus is implicated
CC in numerous human diseases, including cellulitis, eyelid infections, food
CC poisoning, osteomyelitis, skin and surgical wound infections, scalded
CC skin syndrome, toxic shock syndrome, etc. Organisms transformed with the
CC DNA sequences can be used for recombinant production of the polypeptides.
CC The new DNA sequences (and their fragments) are useful as primers or
CC probes for isolating homologues of any of the 5191 S.aureus DNA sequences
CC contained on the computer readable medium
XX
XX Sequence 936 AA;
SQ
Query Match 99.5%; Score 1723; DB 2; Length 936;
Best Local Similarity 99.7%; Pred. No. 3.8e-115;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 VAADAPAGTDTITNQLTNVTVGIDSGTTVYPHQAQYVKLANYGFSVPNSAVKGDTFKITVP 61
DB 230 VAADAPAGTDTITNQLTNVTVGIDSGTTVYPHQAQYVKLANYGFSVPNSAVKGDTFKITVP 289
QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFIDYVNTKDDVKATLTMPAYID 121
DB 290 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFIDYVNTKDDVKATLTMPAYID 349
QY 122 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 181
DB 350 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 409
QY 182 NPSGDNVIAPVLTGNLKPNTDSNALIDQONTSIKVKYKVDNAADLSESYFVNPNFEDVTN 241
DB 410 NPSGDNVIAPVLTGNLKPNTDSNALIDQONTSIKVKYKVDNAADLSESYFVNPNFEDVTN 469
QY 242 SVNITFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGYSNIIWRS 301
DB 470 SVNITFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGYSNIIWRS 529
QY 302 MSWDNEVAFNNGSGSDGIDKPVVPEQPDE 331
DB 530 MSWDNEVAFNNGSGSDGIDKPVVPEQPDE 559
RESULT 9
AAU33975 standard; protein; 1021 AA.
ID AAU33975;
AC AAU33975;
XX 14-FEB-2002 (first entry)
DT
XX Staphylococcus aureus cellular proliferation protein #251.
DE
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
OS Staphylococcus aureus.

XX W0200170955-A2.
XX
XX 27-SEP-2001.
PD
XX 21-MAR-2001; 2001WO-US009180.
PF
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207272P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI
XX
XX WPI: 2001-611495/70.
DR N-PSDB; AAS51834.
DR
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 5471; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIFO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1021 AA;
SQ
Query Match 87.6%; Score 1518; DB 4; Length 1021;
Best Local Similarity 87.3%; Pred. No. 2.3e-100;
Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 2 VAADAPAGTDTITNQLTNVTVGIDSGTTVYPHQAQYVKLANYGFSVPNSAVKGDTFKITVP 61
DB 221 VAADAPAGTDTITNQLTDVKVTIDSGTTVYPHQAQYVKLANYGFSVPNSAVKGDTFKITVP 280
QY 62 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFIDYVNTKDDVKATLTMPAYID 121
DB 281 KELNLNGVTSTAKVPPIMAGDQVLANGVIDSDGNVIYTFIDYVNTKDDVKATLTMPAYID 340
QY 122 PENVKKTGNVTLATGIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 181
DB 341 PENVKKTGNVTLTGIGTNTASKTVLVDEYKYGQFHNLSIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAPVLTGNLKPNTDSNALIDQONTSIKVKYKVDNAADLSESYFVNPNFEDVTN 241
DB 401 NPSGDNVLPALTGNLIPNTKSNALIDAKTIDIKVYRVNDANLSESYFVNPSDFEDVTN 460
QY 242 SVNITFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGDALRSTLYGYSNIIWRS 301
DB 461 QVRISFPNANQYKVEFNTPDQITTPYIVVNGHIDPASTGDLALRSTFYGYDSNFIWRS 520


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OY      302 MSWDNEVAFNNGSGSGDGDIDKPVVPPEQDPDE 331
        |||
DB       521 MSWDNEVAFNNGSGSGDGDIDKPVVPPEQDPDE 550

RESULT 10
ID      AAU36951 standard; protein; 1021 AA.
XX      AAU36951;
AC      AAU36951;
XX      14-FEB-2002 (first entry)
DT
XX      Staphylococcus aureus cellular proliferation protein #1121.
DE
XX      Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW      antibacterial; drug design.
XX
OS      Staphylococcus aureus.
XX      WO200170955-A2.
PN
PD      27-SEP-2001.
XX
PF      21-MAR-2001; 2001WO-US009180.
XX
PR      21-MAR-2000; 2000US-0191078P.
PR      23-MAY-2000; 2000US-0206848P.
PR      26-MAY-2000; 2000US-0207727P.
PR      23-OCT-2000; 2000US-0242578P.
PR      27-NOV-2000; 2000US-0253625P.
PR      22-DEC-2000; 2000US-0257931P.
PR      16-FEB-2001; 2001US-0269308P.
XX
PA      (ELIT-) ELITRA PHARM INC.
XX
PI      Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI      Yamamoto RT, Xu HH;
XX
DR      WPI: 2001-611495/70.
XX      N-PSDB; AAS54810.
XX
PT      New polynucleotides for the identification and development of
PT      antibiotics, comprise sequences of antisense nucleic acids.
XX
PS      Example 3; SEQ ID NO 12544; 511pp; English.
XX
CC      The invention relates to antisense inhibitors of genes essential to
CC      prokaryotic cellular proliferation, their use in identifying the genes,
CC      their use in the discovery of novel antibiotics, the essential genes
CC      themselves and the encoded proteins. The prokaryotes used are Escherichia
CC      coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC      Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC      useful for the identification of potential new targets for antibiotic
CC      development. The antisense nucleic acids can also be used to identify
CC      proteins used in proliferation, to express these proteins, and to obtain
CC      antibodies capable of binding to the expressed proteins. The proteins can
CC      be used to screen compounds in rational drug discovery programmes. The
CC      antisense nucleic acid sequence is also useful to screen for homologous
CC      nucleic acids which are required for cell proliferation in a wide variety
CC      of organisms. The present sequence represents an essential prokaryotic
CC      cellular proliferation protein. Note: The sequence data for this patent
CC      did not form part of the printed specification, but was obtained in
CC      electronic format directly from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 1021 AA;

Query Match          87.6%; Score 1518; DB 4; Length 1021;
Best Local Similarity 87.3%; Pred. No. 2.3e-100;
Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

```

Db	221	VAADAPAGTDITNQLTDVYKVTIIDSCTTVYPHQAGYVKLNKGEVSVENSAVKGDTFKITVP	280
QY	62	KELNLNGVTSTAKVPPIMAGDOVLANGVIDSDGNVIYTFDYYNTKDDYKATLTMPAYID	121
Db	281	KELNLNGVTSTAKVPPIMAGDOVLANGVIDSDGNVIYTFDYYNTKENVANTANITMPAYID	340
QY	122	PENVKKTGNVTLATGISTANKVLVDYEKYGKFPYNLSIKGTIDQIDKTNNTYRQTIYV	181
Db	341	PENVTKTGNVTLTGTIGTNTASKTVLIDYEKYGQFHNLSIKGTIDQIDKTNNTYRQTIYV	400
QY	182	NPSGDNVIAPVLTGNLKPNTBSNALIDQONTSIKVYKVDNAADLSSESYFVNPNFEDVTN	241
Db	401	NPSGDNVVLPAITGNLIPNTXSNALIDAKNTDIKVYRVNDANLDSSESYVNPBDSFEDVTN	460
QY	242	SVNITFPNPNOYKVEFNTPPDOITTPYIVVWNGHIDPNSKGLALRSTLYGYSNIIWRS	301
Db	461	QVRISFPNANQYKVEFFTDQDQITTPYIVVWNGHIDPASTGLALRSTFYGYDSNFIWRS	520
QY	302	MSWDNEVAFNNGSGSGDGDIDKPVVPEQPD	331
Db	521	MSWDNEVAFNNGSGSGDGDIDKPVVPEQPD	550

RESULT 11
 ABU16402
 ID ABU16402 standard; protein; 935 AA.
 XX
 AC ABU16402;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #1929.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Staphylococcus aureus.
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA20272.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 44326; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 935 AA;

SQ Query Match 87.6%; Score 1517; DB 6; Length 935;

Best Local Similarity 87.3%; Pred. No. 2.4e-100;

Matches 288; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNQLTNVTVGIDSGTIVPHQAGYVKLNFGFSVNSAVKGDTFKITVP 61
DB 221 VAADAPAGTDTITNQLTNVTVGIDSGTIVPHQAGYVKLNFGFSVNSAVKGDTFKITVP 280
QY 62 KELNLNGVTSTAKVPIIMAGDQVLANGVIDSDGNVIYFTDYVNTKDDVKATLTMPAYID 121
DB 281 KELNLNGVTSTAKVPIIMAGDQVLANGVIDSDGNVIYFTDYVNTKDDVKATLTMPAYID 340
QY 122 PENVKKTGNVTLATIGSTTANKTVLVDEYKKGKFNLSIKGTIDQIDKTNNTYRQTIYV 181
DB 341 PENVKKTGNVTLATIGSTTANKTVLVDEYKKGKGFHNLISIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAPVLITGNLKPNTDSNALIDQNTSIKVKYKVDNADLSSESYFVNPNFEDVTN 241
DB 401 NPSGDNVLPALITGNLIPNTKSNALIDAKNTDIKVRVDNANDLSSESYVNPSPFEDVTN 460
QY 242 SVNITFPNPQYKVEFNTPDQITTPYIVVNGHIDPNSKGLALRSTLYGYSNIIWRS 301
DB 461 QVRISFPNANQYKVEFNTPDQITTPYIVVNGHIDPASTGDLALRSTFYGYDSNFIWRS 520
QY 302 MSWDNEVAFNNGSGSDGIDKPVVPEQPDE 331
DB 521 MSWDNEVAFNNGSGSDGIDKPVVPEQPDE 550

RESULT 12

AAU75490 standard; protein; 496 AA.

AC AAU75490;

DT 23-APR-2002 (first entry)

DE *S. aureus* antigenic protein associated protein #10.

XX Antigenic protein; vaccine; SEREX; antibacterial; antiinflammatory;
KM dermatological; antitumor; tuberculostatic; immunosuppressive;
KM septicemia; food poisoning; skin disorders; peritonitis; endocarditis;
KM tuberculosis; blood infection; sepsis; meningitis; pneumonia;
KM stomach ulcer; gonorrhea; necrotising fasciitis; impetigo;
KM Lyme's disease; gastro-enteritis; dysentery; shigellosis.

OS Staphylococcus aureus.

PN WO200198499-A1.
PD 27-DEC-2001.
XX 20-JUN-2001; 2001WO-GB002685.
PF 20-JUN-2000; 2000GB-00014907.
XX 20-JUN-2000; 2000GB-00014907.
PR (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
XX Foster S, McDowell P, Brummell K, Clarke S;
PI WPI; 2002-106544/14.
DR
XX Identifying antigenic polypeptides expressed by pathogenic organisms
PT e.g., *Staphylococcus aureus* during infection, by SEREX (serological
PT identification of antigens by recombinant expression cloning) techniques.
XX Disclosure; Page 72-74; 85pp; English.

XX The invention relates to a method for identifying antigenic polypeptides
CC expressed by pathogenic organisms e.g., *Staphylococcus aureus* during
CC infection, by SEREX (serological identification of antigens by
CC recombinant expression cloning) techniques. The method involves providing
CC a nucleic acid library encoding genes/partial gene sequences of
CC pathogenic organisms, transforming/transfecting the library into host
CC cells, contacting the polypeptides expressed by the genes with autologous
CC antisera derived from an animal infected with, or has been infected with
CC the pathogen and purifying the nucleic acid encoding the polypeptide or
CC partial polypeptide binding to the antisera. Also included are the
CC nucleic acids and polypeptides isolated by the method, vectors and
CC transformed cells expressing them, a vaccine comprising the polypeptide
CC and the production of monoclonal antibodies against the polypeptides. The
CC protein and vaccine are useful for immunising an animal (preferably
CC human) against a pathogenic microbe. The proteins and antibodies are
CC useful for manufacturing a medicament for treating *Staphylococcus aureus*-
CC associated septicemia, food poisoning or skin disorders or
CC *Staphylococcus epidermidis*-associated septicemia, sepsis, meningitis,
CC endocarditis, tuberculosis, blood infections, peritonitis,
CC pneumonia, stomach ulcers, gonorrhea, necrotising fasciitis, impetigo,
CC Lyme's disease, gastro-enteritis, dysentery and shigellosis. The present
CC sequence is an *S. aureus* protein sequence associated with the antigenic
CC proteins of the invention. Note: The present sequence is included in the
CC sequence listing but is not mentioned anywhere else in the specification

XX Sequence 496 AA;

Query Match 82.7%; Score 1433; DB 5; Length 496;

Best Local Similarity 100.0%; Pred. No. 1.1e-94;

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNQLTNVTVGIDSGTIVPHQAGYVKLNFGFSVNSAVKGDTFKITVP 61
DB 221 VAADAPAGTDTITNQLTNVTVGIDSGTIVPHQAGYVKLNFGFSVNSAVKGDTFKITVP 280
QY 62 KELNLNGVTSTAKVPIIMAGDQVLANGVIDSDGNVIYFTDYVNTKDDVKATLTMPAYID 121
DB 281 KELNLNGVTSTAKVPIIMAGDQVLANGVIDSDGNVIYFTDYVNTKDDVKATLTMPAYID 340
QY 122 PENVKKTGNVTLATIGSTTANKTVLVDEYKKGKFNLSIKGTIDQIDKTNNTYRQTIYV 181
DB 341 PENVKKTGNVTLATIGSTTANKTVLVDEYKKGKGFHNLISIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAPVLITGNLKPNTDSNALIDQNTSIKVKYKVDNADLSSESYFVNPNFEDVTN 241
DB 401 NPSGDNVIAPVLITGNLKPNTDSNALIDQNTSIKVKYKVDNADLSSESYFVNPNFEDVTN 460
QY 242 SVNITFPNPQYKVEFNTPDQITTPYIVVNGHID 277
DB 461 SVNITFPNPQYKVEFNTPDQITTPYIVVNGHID 496

RESULT 13
ADA89664
ID ADA89664 standard; protein; 496 AA.
XX
AC ADA89664;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus antigenic protein #203.
XX
antigenic protein; vaccine; Staphylococcus aureus; pathogenic organism;
KM antibacterial; neuroprotective; immunosuppressive; antiinflammatory;
KM antiulcer; immunostimulant; ophthalmological; pathogenic microbe;
KM bacteraemia; septic shock; organ infection; skin infection;
KM bacterial basal colonisation; bacterial eye infection; septicaemia;
KM tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
KM sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
KM necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
KM gastro-enteritis; dysentery; shigellosis; skin disorder.
XX
OS Staphylococcus aureus.
XX
PN WO2003011899-A2.
XX
PD 13-FEB-2003.
XX
PF 02-AUG-2002; 2002WO-GB003606.
XX
PR 02-AUG-2001; 2001GB-00018825.
PR 09-JAN-2002; 2002GB-00000349.
XX
PA (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
XX
PI Foster S, Mond J, Clarke S, McDowell P, Brummel K;
XX
DR WPI; 2003-256434/25.
XX
DT New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
PT useful as a vaccine for immunizing humans against e.g. bacteremia, septic
PT shock, septicemia, tuberculosis, meningitis, pneumonia, gonorrhea or
PT impetigo.
XX
PS Claim 4; Page 161; 189pp; English.
XX
The present invention describes an antigenic protein or its part, which
is for use as a vaccine. The antigenic protein is encoded by an isolated
DNA molecule of Staphylococcus aureus or S. epidermidis partial gene
sequences (designated dnaSA and dna SE, respectively; and which encodes a
protein expressed by a pathogenic organism. Also described: (1) a vaccine
composition comprising at least one antigenic protein; (2) a method of
immunising an animal against a disease or condition caused by a
pathogenic microbe by administering the antigenic protein or the vaccine;
(3) an antibody or its binding part obtainable by the method above; (4)
preparing a hybridoma cell line producing monoclonal antibodies; (5) a
hybridoma cell line produced by the method of (4); and (6) identifying
opsonic antigens expressed by a pathogenic microbe. The antigenic
proteins have antibacterial, neuroprotective, immunosuppressive,
antiinflammatory, antiulcer, immunostimulant and ophthalmological
activities, and can be used in vaccines. The antigenic proteins or
vaccines can be used for immunising an animal (specifically a human)
against a disease or condition caused by a pathogenic microbe, e.g.
bacteraemia, septic shock, organ infection, skin infection, bacterial
basal colonisation, bacterial eye infections, septicaemia, tuberculosis,
bacteria-associated food poisoning, blood infections, peritonitis,
endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea,
strep throat, streptococcal-associated toxic shock, necrotising
fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,
dysentery, shigellosis, S. aureus-associated septicaemia, food-poisoning,
skin disorders, S. epidermidis-associated septicaemia, peritonitis or
endocarditis. The present sequence represents a S. aureus antigenic
protein sequence from the present invention.

Sequence 496 AA;
Query Match 82.7%; Score 1433; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.1e-94;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAADAPAACTDITNQLTNVTVGIDSGTTVYPHQAQVYKLNFGSPVPSAVKGDTEKITVP 61
DB 221 VAADAPAACTDITNQLTNVTVGIDSGTTVYPHQAQVYKLNFGSPVPSAVKGDTEKITVP 280
QY 62 KEINLVGVSTAKVPPIMAGDQVLANGVIDSDGNVYFTFDYVNTKDVKATLTMPAYID 121
DB 281 KEINLVGVSTAKVPPIMAGDQVLANGVIDSDGNVYFTFDYVNTKDVKATLTMPAYID 340
QY 122 PENVKKTNVTLATIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKNNTRYQTIYV 181
DB 341 PENVKKTNVTLATIGSTTANKTVLVDEYKYGKFNLSIKGTIDQIDKNNTRYQTIYV 400
QY 182 NPSGDNVIAFVLTKNPKPNTDSNALIDQNTSIKYYKVDNAADLSESYFVNPFEDVTN 241
DB 401 NPSGDNVIAFVLTKNPKPNTDSNALIDQNTSIKYYKVDNAADLSESYFVNPFEDVTN 460
QY 242 SVNITFENPNQYKVEFNTPDQITTPYIVVNGHID 277
DB 461 SVNITFENPNQYKVEFNTPDQITTPYIVVNGHID 496
RESULT 14
ADA89663
ID ADA89663 standard; protein; 496 AA.
XX
AC ADA89663;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus antigenic protein #202.
XX
KM antigenic protein; vaccine; Staphylococcus aureus; pathogenic organism;
KM antibacterial; neuroprotective; immunosuppressive; antiinflammatory;
KM antiulcer; immunostimulant; ophthalmological; pathogenic microbe;
KM bacteraemia; septic shock; organ infection; skin infection;
KM bacterial basal colonisation; bacterial eye infection; septicaemia;
KM tuberculosis; food poisoning; blood infection; peritonitis; endocarditis;
KM sepsis; meningitis; pneumonia; stomach ulcer; gonorrhoea; toxic shock;
KM necrotising fasciitis; impetigo; histoplasmosis; Lyme disease;
KM gastro-enteritis; dysentery; shigellosis; skin disorder.
XX
OS Staphylococcus aureus.
XX
PN WO2003011899-A2.
XX
PD 13-FEB-2003.
XX
PF 02-AUG-2002; 2002WO-GB003606.
XX
PR 02-AUG-2001; 2001GB-00018825.
PR 09-JAN-2002; 2002GB-00000349.
XX
PA (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
XX
PI Foster S, Mond J, Clarke S, McDowell P, Brummel K;
XX
DR WPI; 2003-256434/25.
XX
DT New antigenic polypeptides from Staphylococcus aureus or S. epidermidis,
PT useful as a vaccine for immunizing humans against e.g. bacteremia, septic
PT shock, septicemia, tuberculosis, meningitis, pneumonia, gonorrhea or
PT impetigo.
XX
PS Claim 4; Page 160-161; 189pp; English.
XX
The present invention describes an antigenic protein or its part, which

CC is for use as a vaccine. The antigenic protein is encoded by an isolated
CC DNA molecule of Staphylococcus aureus or S. epidermidis partial gene
CC sequences (designated dnaA and dna SE, respectively; and which encodes a
CC protein expressed by a pathogenic organism. Also described: (1) a vaccine
CC composition comprising at least one antigenic protein; (2) a method of
CC immunising an animal against a disease or condition caused by a
CC pathogenic microbe by administering the antigenic protein or the vaccine;
CC (3) an antibody or its binding part obtainable by the method above; (4)
CC preparing a hybridoma cell line producing monoclonal antibodies; (5) a
CC hybridoma cell line produced by the method of (4); and (6) identifying
CC opsonic antigens expressed by a pathogenic microbe. The antigenic
CC proteins have antibacterial, neuroprotective, immunosuppressive,
CC antiinflammatory, antitumor, immunostimulant and ophthalmological
CC activities, and can be used in vaccines. The antigenic proteins or
CC vaccines can be used for immunising an animal (specifically a human)
CC against a disease or condition caused by a pathogenic microbe, e.g.
CC bacteraemia, septic shock, organ infection, skin infection, bacterial
CC basal colonisation, bacterial eye infections, septicæmia, tuberculosis,
CC bacteria-associated food poisoning, blood infections, peritonitis,
CC endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea,
CC strept throat, streptococcal-associated toxic shock, necrotising
CC fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis,
CC dysentery, shigellosis, S. aureus-associated septicæmia, food-poisoning,
CC skin disorders, S. epidermidis-associated septicæmia, peritonitis or
CC endocarditis. The present sequence represents a S. aureus antigenic
CC protein sequence from the present invention.

XX SQ Sequence 496 AA;

Query Match 82.7%; Score 1433; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.1e-94;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAADAPAGTDTITNQLTNVTVGIDSGTIVYPHQAGYVKLNYSVNSAVKGDTFKITVP 61
DB 221 VAADAPAGTDTITNQLTNVTVGIDSGTIVYPHQAGYVKLNYSVNSAVKGDTFKITVP 280
QY 62 KELNLNGVSTAKVPPIMAGDQVLANGVILSDGNVIYFTDYVNTKDDVKATLTMPAYTD 121
DB 281 KELNLNGVSTAKVPPIMAGDQVLANGVILSDGNVIYFTDYVNTKDDVKATLTMPAYTD 340
QY 122 PENVKKTGNVLTATGIGSTTANKTVLVDEYKGYKFNLSIKGTIDQIDKTNNTYRQTIYV 181
DB 341 PENVKKTGNVLTATGIGSTTANKTVLVDEYKGYKFNLSIKGTIDQIDKTNNTYRQTIYV 400
QY 182 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYKVDNAADLSESYFVNPENFEDVTN 241
DB 401 NPSGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYKVDNAADLSESYFVNPENFEDVTN 460
QY 242 SVNITFPNPQYKVEFNTPPDDQITTPYIVVNGHID 277
DB 461 SVNITFPNPQYKVEFNTPPDDQITTPYIVVNGHID 496

RESULT 15
ABU15854
ID ABU15854 standard; protein; 961 AA.
XX
AC ABU15854;
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #1381.
XX
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA19724.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 43778; 1766bp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 961 AA;

Query Match 24.0%; Score 416.5; DB 6; Length 961;
Best Local Similarity 29.1%; Pred. No. 2.9e-21;
Matches 101; Conservative 69; Mismatches 144; Indels 33; Gaps 9;

QY 2 VAADAPAGTDTITNQLTNVTVGID----SGTIVYPHQAGYVKLNYSVNSAVKGDTFK 57
DB 158 VAEEAKATGTDVTKYVETLESSLEGHNKDSNIVNPHNAQRVTLKYKWEFEGEIKAGDYFD 217
QY 58 ITVPKELNLNGVSTAKVPPIMAG--DOVLANGVIDSDGNVIYFTDYVNTKDDVKATLT 115
DB 218 FTLSDNVETHGISLTKRYPEIKSSTEDKVMANGQVINERTIRYFTDYINNKKDLTAELN 277
QY 116 MEAYIDPENVKKTGNVLTATGIGSTTANKTVLVY-----EKYKGFYNLSIKGTIDQIDK 170
DB 278 LNLFDFTVTVKQSGQKVEVTLGQNKVSKEPDIKYLGVKDRMG-----VTVNGRIDTLNK 333
QY 171 TNNTYRQTIYVNPESGDNVIAPVLTGNLKPNTDSNALIDQNTSIKVKYKVDNAADLSESYF 230

Db 334 BEGKFSHFAYVKPNNQSLTSVTVTGQVTSGYKQSA---NPTVKYKYKHIGSDELAESVY 389
QY 231 V---NPNFEDVTNSVNI TFPNPNOYKVEFNTPDQITTPYIVVNGHIDPNSKGLALR 287
Db 390 AKLDDTSKFEDVTEKVNLSYTSNGGYTLNLGLDND--SKDYVIRYEGEYDQNAK-DLNR 446
QY 288 STLYGYNSNIWR-----SMSWDNEVAFNNGSGSGDGIDKPVVP 326
Db 447 THLSGYHKYYPYYPYYPVQLTWNGVAFYSNNAKGDGDKPNDP 493

Search completed: March 26, 2004, 05:03:55
Job time : 130.592 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 05:00:12 ; Search time 34.6259 Seconds
(without alignments)
493.509 Million cell updates/sec

Title: US-10-056-052A-4
Perfect score: 1732
Sequence: 1 MVADAPAPAGTDTNQLTNV.....NGSGSGDIDKPVPEQPD 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1732	100.0	345	US-08-856-253-7	Sequence 7, Appl1
2	1727	99.7	933	US-08-293-728-2	Sequence 2, Appl1
3	1727	99.7	933	US-09-421-868-2	Sequence 2, Appl1
4	1723	99.5	936	US-08-956-171B-5249	Sequence 5249, Ap
5	353	20.4	930	US-09-134-001C-5314	Sequence 5314, Ap
6	353	20.4	930	US-09-386-962C-10	Sequence 10, Appl
7	331	19.1	1027	US-08-956-171B-5254	Sequence 5254, Ap
8	323.5	18.7	1166	US-09-200-650E-7	Sequence 7, Appl1
9	312.5	18.0	918	US-09-200-650E-1	Sequence 1, Appl1
10	282.5	16.3	251	US-08-956-171E-5252	Sequence 5252, Ap
11	257.5	14.9	1315	US-09-200-650E-5	Sequence 5, Appl1
12	210.5	12.2	930	US-09-200-650E-3	Sequence 3, Appl1
13	204	11.8	1112	US-08-714-402-2	Sequence 2, Appl1
14	204	11.8	1161	US-09-327-536-2	Sequence 2, Appl1
15	201.5	11.6	1742	US-09-386-962C-4	Sequence 4, Appl1
16	139.5	8.1	368	US-09-134-000C-4597	Sequence 4597, Ap
17	136	7.9	559	US-08-956-171E-5251	Sequence 5251, Ap
18	131	7.6	2504	US-09-328-352-5821	Sequence 5821, Ap
19	129.5	7.5	1216	US-09-134-000C-5130	Sequence 5130, Ap
20	129.5	7.4	1391	US-10-080-505-11	Sequence 11, Appl
21	127.5	7.2	1391	US-10-080-505-15	Sequence 15, Appl
22	124.5	7.1	1411	US-10-080-505-17	Sequence 17, Appl
23	123.5	7.1	731	US-09-107-532A-6999	Sequence 6999, Ap
24	123	7.1	2385	US-09-543-681A-6304	Sequence 6304, Ap
25	122.5	7.0	992	US-09-206-942-61	Sequence 61, Appl
26	121.5	7.0	998	US-09-206-942-59	Sequence 59, Appl
27	121.5	7.0			

28	120.5	7.0	920	4	US-09-463-402-6	Sequence 6, Appl1
29	120.5	7.0	921	4	US-09-889-572-4	Sequence 4, Appl1
30	120	6.9	737	4	US-09-071-035-460	Sequence 460, App
31	120	6.9	2032	4	US-09-071-035-458	Sequence 458, App
32	120	6.9	2032	4	US-09-071-035-462	Sequence 462, App
33	120	6.9	2032	4	US-09-071-035-466	Sequence 466, App
34	120	6.9	2054	4	US-09-134-000C-6612	Sequence 6612, Ap
35	118	6.8	789	4	US-09-002-285-94	Sequence 94, Appl
36	118	6.8	789	4	US-09-589-477-94	Sequence 94, Appl
37	117	6.8	1180	4	US-09-206-942-65	Sequence 65, Appl
38	117	6.8	1188	4	US-09-206-942-63	Sequence 63, Appl
39	116	6.7	789	4	US-09-002-285-96	Sequence 96, Appl
40	116	6.7	789	4	US-09-589-477-96	Sequence 96, Appl
41	116	6.7	3892	4	US-09-328-352-5503	Sequence 5503, Ap
42	115.5	6.7	405	4	US-09-328-352-5300	Sequence 5300, Ap
43	115.5	6.7	949	4	US-09-198-452A-478	Sequence 478, App
44	115	6.6	790	3	US-08-960-780-4	Sequence 4, Appl1
45	115	6.6	790	3	US-09-073-898-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-856-253-7
Sequence 7, Application US/08856253
Patent No. 6288214
GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Sthanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-856-253-7

Query Match 100.0%; Score 1732; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	I	MVADAPAGT	DI	TNQLTNV	TG	IGDSG	TV	PHQAGY	KUN	YGS	V	SPNSA	VKGD	TEKIT	IV	60																																										
Db	13	MVADAPAGT	DI	TNQLTNV	TG	IGDSG	TV	PHQAGY	KUN	YGS	V	SPNSA	VKGD	TEKIT	IV	72																																										
QY	61	PKE	L	N	G	V	T	S	T	A	K	V	P	I	M	A	G	D	Q	V	L	A	N	G	V	I	D	S	D	G	N	V	I	T	F	I	D	V	N	T	K	D	V	K	A	T	L	M	P	A	Y	I	120					
Db	73	PKE	L	N	G	V	T	S	T	A	K	V	P	I	M	A	G	D	Q	V	L	A	N	G	V	I	D	S	D	G	N	V	I	T	F	I	D	V	N	T	K	D	V	K	A	T	L	M	P	A	Y	I	132					
QY	121	D	P	E	N	V	K	T	G	N	V	T	L	A	T	G	I	G	S	T	T	A	N	K	T	V	L	V	D	E	K	Y	K	G	F	Y	N	L	S	I	K	G	T	I	D	I	D	K	T	N	T	Y	R	O	T	I	Y	180
Db	133	D	P	E	N	V	K	T	G	N	V	T	L	A	T	G	I	G	S	T	T	A	N	K	T	V	L	V	D	E	K	Y	K	G	F	Y	N	L	S	I	K	G	T	I	D	I	D	K	T	N	T	Y	R	O	T	I	Y	192
QY	181	V	N	P	S	G	D	N	V	I	A	P	V	L	T	G	N	L	K	P	N	T	S	N	A	L	I	D	Q	N	T	S	I	K	V	Y	K	V	D	N	A	D	L	S	E	S	Y	F	V	N	P	E	N	E	D	V	T	240
Db	193	V	N	P	S	G	D	N	V	I	A	P	V	L	T	G	N	L	K	P	N	T	S	N	A	L	I	D	Q	N	T	S	I	K	V	Y	K	V	D	N	A	D	L	S	E	S	Y	F	V	N	P	E	N	E	D	V	T	252
QY	241	N	S	V	N	I	T	F	P	N	Q	Y	K	V	E	N	T	P	D	D	I	T	P	Y	I	V	V	N	G	H	I	D	P	N	S	K	G	D	L	A	R	S	T	L	Y	G	Y	N	S	N	I	I	M	R	300			
Db	253	N	S	V	N	I	T	F	P	N	Q	Y	K	V	E	N	T	P	D	D	I	T	P	Y	I	V	V	N	G	H	I	D	P	N	S	K	G	D	L	A	R	S	T	L	Y	G	Y	N	S	N	I	I	M	R	312			
QY	301	S	M	S	W	D	N	E	V	A	F	N	N	G	S	G	S	G	D	G	I	D	K	P	V	P	E	Q	P	D	E	331																										
Db	313	S	M	S	W	D	N	E	V	A	F	N	N	G	S	G	S	G	D	G	I	D	K	P	V	P	E	Q	P	D	E	343																										

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RESULT 2
US-08-293-728-2
; Sequence 2, Application US/08293728D
; Patent No. 6008341
; GENERAL INFORMATION:
; APPLICANT: Foster, Timothy J.
; APPLICANT: McDevitt, Damien L.
; TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene
; FILE REFERENCE: 05344.105011
; CURRENT APPLICATION NUMBER: US/08/293,728D
; CURRENT FILING DATE: 1994-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-293-728-2

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Query Match	99.7%;	Score 1727;	DB 3;	Length 933;
Best Local Similarity	100.0%;	Pred. No. 1.9e-141;		
Matches 330; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	Z	VADAPABA	GTDITNQLTNVTVGIDSGTITYYPHQA	GVKLN	GFSPNSA	YKGDTEKITVP	61
Db	221	VAADAPAAGT	DITNQLTNVTVGIDSGTITYYPHQAGV	KLN	GFSPNSA	YKGDTEKITVP	280
QY	62	KELNLNGVT	STAKVPPIMAGDOVLANGVIDSDGNVIYTFTDYNTK	DDYKATLTM	PAYID		121
Db	281	KELNLNGVT	STAKVPPIMAGDOVLANGVIDSDGNVIYTFTDYNTK	DDYKATLTM	PAYID		340
QY	122	PENVKKTGNVT	LATIGISTTANKTVLVDEYKKGKFYNLSIKGTIDQIDKTNNTYRQTIIY				181
Db	341	PENVKKTGNVT	LATIGISTTANKTVLVDEYKKGKFYNLSIKGTIDQIDKTNNTYRQTIIY				400
QY	182	NPSGDNVAI	FVLGNLKPN	TDSNALIDQONTSIKYKV	DNAADLSES	YFVNPFEDVTN	241
Db	401	NPSGDNVAI	FVLGNLKPN	TDSNALIDQONTSIKYKV	DNAADLSES	YFVNPFEDVTN	460
QY	242	SVNITFPNPNOYKVE	FNTPDDQITTPYIVVVNGHI	DSPNSKGLALRSTLYGYSN	NIWRS		301
Db	461	SVNITFPNPNOYKVE	FNTPDDQITTPYIVVVNGHI	DSPNSKGLALRSTLYGYSN	NIWRS		520
QY	302	MSWDNEVA	FNNSSGSDGIDKPVPPEQPDE				331
Db	521	MSWDNEVA	FNNSSGSDGIDKPVPPEQPDE				550

```

RESULT 3
US-09-421-868-2
; Sequence 2, Application US/09421868
; Patent No. 6177084
; GENERAL INFORMATION:
; APPLICANT: Foster, Timothy J.
; APPLICANT: McDevitt, Damien L.
; -TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene
; FILE REFERENCE: 05344.105011
; CURRENT APPLICATION NUMBER: US/09/421, 868
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 08/293,728
; PRIOR FILING DATE: 1994-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-421-868-2

```

```

Query Match      . 99.7%; Score 1727; DB 3; Length 933;
Best Local Similarity 100.0%; Pred. No. 1.9e-141;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	2	VAADAPAGT	DITN	QLTN	VTVG	IDSG	TTVY	PHQAGY	YKLN	GER	SV	PN	SA	VK	GD	T	F	K	I	T	V	P	61		
Db	221	VAADAPAGT	DITN	QLTN	VTVG	IDSG	TTVY	PHQAGY	YKLN	GER	SV	PN	SA	VK	GD	T	F	K	I	T	V	P	280		
QY	62	KELNLNGV	T	STAK	V	P	I	MAGD	QV	L	ANG	V	I	D	S	D	G	N	V	I	T	F	T	Y	121
Db	281	KELNLNGV	T	STAK	V	P	I	MAGD	QV	L	ANG	V	I	D	S	D	G	N	V	I	T	F	T	Y	340
QY	122	PENVKKTGN	V	T	L	A	T	G	I	S	T	T	A	N	K	T	V	L	V	D	E	K	Y	K	161
Db	341	PENVKKTGN	V	T	L	A	T	G	I	S	T	T	A	N	K	T	V	L	V	D	E	K	Y	K	400
QY	182	NPSGDNV	I	A	P	V	L	T	G	N	L	K	P	N	T	S	N	A	L	I	D	Q	N	T	241
Db	401	NPSGDNV	I	A	P	V	L	T	G	N	L	K	P	N	T	S	N	A	L	I	D	Q	N	T	460
QY	242	SVNITF	P	N	P	N	Q	K	V	E	F	N	T	P	D	Q	I	T	T	P	Y	I	V	301	
Db	461	SVNITF	P	N	P	N	Q	K	V	E	F	N	T	P	D	Q	I	T	T	P	Y	I	V	520	
QY	302	MSMDNEV	A	F	N	N	G	S	G	D	G	I	D	K	P	V	V	E	Q	P	D	E			
Db	521	MSMDNEV	A	F	N	N	G	S	G	D	G	I	D	K	P	V	V	E	Q	P	D	E			

RESULT 4
 US-08-956-171E-5249
 ; Sequence 5249, Application US/08956171E
 ; Patent No. 6593114
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Charles Kunsch
 ; Gil H. Choi
 ; Patrick S. Dillon
 ; Craig A. Rosen
 ; Steven C. Barash
 ; Michael R. Fannon
 ;
 ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 ;
 ; NUMBER OF SEQUENCES: 5256
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ;
 ; COMPUTER READABLE FORM:
 ;
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 ;

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; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 936 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5249:
US-08-956-171E-5249

Query Match          99.5%; Score 1723; DB 4; Length 936;
Best Local Similarity 99.7%; Pred. No. 4.3e-141;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VAADAPAGTDITNQLTNTVTVGIDSGTTVYPHQAQYKLNFGSVSPNSAVKGDTEKITVP 61
   |||||
Db 230 VAADAPVAGTDITNQLTNTVTVGIDSGTTVYPHQAQYKLNFGSVSPNSAVKGDTEKITVP 289

QY 62 KELNLNGVTSTAKVPRIMAGDQVLANGVIDSDGNVYTFETDYVNTKDPYKATLTMPAYID 121
   |||||
Db 290 KELNLNGVTSTAKVPRIMAGDQVLANGVIDSDGNVYTFETDYVNTKDPYKATLTMPAYID 349

QY 122 PENVKKTGNTLATGISTTANKTVLVVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 181
   |||||
Db 350 PENVKKTGNTLATGISTTANKTVLVVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYV 409

QY 182 NPSGDNVIAPVLTGNLKPNLDSNALIDQNTSIRKYKYVDNAADLSESYFVNPENFEDVTN 241
   |||||
Db 410 NPSGDNVIAPVLTGNLKPNLDSNALIDQNTSIRKYKYVDNAADLSESYFVNPENFEDVTN 469

QY 242 SVNITFPNPNOYKVEFNPDPDQITTPYIVVNGHIDPNSKGDLLRSTLYGNSNIWRS 301
   |||||
Db 470 SVNITFPNPNOYKVEFNPDPDQITTPYIVVNGHIDPNSKGDLLRSTLYGNSNIWRS 529

QY 302 MSWDNEVAFNNGSGSGDGIKPVVPEQPDE 331
   |||||
Db 530 MSWDNEVAFNNGSGSGDGIKPVVPEQPDE 559

RESULT 5
US-09-134-001C-5314
; Sequence 5314, Application US/091344001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
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; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5314
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5314

Query Match          20.4%; Score 353; DB 4; Length 930;
Best Local Similarity 30.6%; Pred. No. 4.7e-22;
Matches 101; Conservative 60; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLTNTVGI-DSGTTVYPHQAQYKLNFGSVSPNSAVKGDTEKITVPKELNLNGVTS 71
   :||:
Db 284 VTDQ--SITEGYDSDGIIKAHDAENLIYDVFVDDKVKSGDTMTVNIIDKNTVPSDLTD 341

QY 72 TAKVPRIMAGD-QVLANGVID-SDGNVYTFETDYVNTKDPYKATLTMPAYIDPENVKKTG 129
   :||:
Db 342 SFAIPKIDNSGEIATGTVDNTNKQITFTFDYDKYENIKAHKLKLSYIDSKVPNNN 401

QY 130 ---NVTLATGISTTANKTVLVVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYVNPESGD 186
   :||:
Db 402 TKLDVEYKTAI--VNKTIIVYQKPNENRTANLQSMFTNIDTKHTEQTIYINPL-- 457

QY 187 NVIAPVLTGNLKPNLDSNALIDQNTSIRKYKYVDNAADLSESYFV-NPENFEDVTSVNI 245
   |||||
Db 458 RYSAKETNWNISGNGDEGSTITIDSTIIKYKVGDNQNLPSNRIDYSEYEDVTNDQYA 517

QY 246 TRPNPNQYKVEFNPDPDQITTPYIVVNGHIDPNSKGD-----LALRSTLYGNSNII 298
   |||||
Db 518 QLGNNNDVNINFG---NIDSPYIIKVISKYDEN-KDDYTTIQGTVMQTINNEYTGE-- 570

QY 299 WRSMWDNEVAFNNGSGSGDGIKPVVPEQ 328
   :||:
Db 571 FRITASYNNTIAFSTSSGQCG-DLP--PEK 597

RESULT 6
US-09-386-962C-10
; Sequence 10, Application US/09386962C
; Patent No. 6635473
; GENERAL INFORMATION:
; APPLICANT: FOSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCUS
; FILE REFERENCE: P06335US2/BAS
; CURRENT APPLICATION NUMBER: US/09/386,962C
; CURRENT FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-386-962C-10

Query Match          20.4%; Score 353; DB 4; Length 930;
Best Local Similarity 30.6%; Pred. No. 4.7e-22;
Matches 101; Conservative 60; Mismatches 139; Indels 30; Gaps 14;

QY 13 ITNQLTNTVGI-DSGTTVYPHQAQYKLNFGSVSPNSAVKGDTEKITVPKELNLNGVTS 71
   :||:
Db 284 VTDQ--SITEGYDSDGIIKAHDAENLIYDVFVDDKVKSGDTMTVNIIDKNTVPSDLTD 341

QY 72 TAKVPRIMAGD-QVLANGVID-SDGNVYTFETDYVNTKDPYKATLTMPAYIDPENVKKTG 129
   :||:
Db 342 SFAIPKIDNSGEIATGTVDNTNKQITFTFDYDKYENIKAHKLKLSYIDSKVPNNN 401

QY 130 ---NVTLATGISTTANKTVLVVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYVNPESGD 186
   :||:
Db 402 TKLDVEYKTAI--VNKTIIVYQKPNENRTANLQSMFTNIDTKHTEQTIYINPL-- 457
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QY 187 NVIAFVLTLGNLKPNTDSNALIDQNTSIRKYKVDNAADLSESYFV-NPENFEDVTNSVNI 245
DB 458 RYSAKETNVNISGNGDEGSTITIDSTIIKVKVGDNONLPDSNRIYDYSEYEDVTNDDYA 517
QY 246 TFPNPNQYKVEFNTPPDQITTPYIVVNGHIDPNSKGD-----LALRSTLYGYSNII 298
DB 518 QIGNNNDVNINFG---NIDSPYIIKVISKYDPN-KDYTTTICQTVTMQTTINEYTG-- 570
QY 299 WRSMWDNEVAFNNGSGSGDIDKPVPEQ 328
DB 571 FRTASYDNITAFSTSSGGQG-DLP--PEK 597

RESULT 7

US-08-956-171E-5254
; Sequence 5254, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch

; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5254:
SEQUENCE CHARACTERISTICS:
LENGTH: 1027 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5254:
us-08-956-171E-5254

Query Match 19.1%; Score 331; DB 4; Length 1027;
Best Local Similarity 24.6%; Pred. No. 4.4e-20;
Matches 82; Conservative 77; Mismatches 146; Indels 28; Gaps 11;

QY 10 GTDITNQLTNVTGIDSG---TTVPYHQAGYKLNFGFVSPNSAVKGDITFKITVPKELN 65
DB 203 GTDVTSKVT-VEIGSIEGHNNNTNKVEPHAGQRAVLKYLKKEENGLHQGDYDFDTLSNNVN 261

QY 66 LINGVTSTAKVPPIMAGDQVLANGVIDSDGNVITFTDYVNTKDDVKATLTMFAYIDPENV 125
DB 262 THGVSTARKVPEIKNGSVWATGEVLEGGKIRYFTFTNDIEDKVDTAELEINLFIIDPKTV 321
QY 126 KKTGNVTLATGIGSTTANKTVLVYD-EKYGKFYNISIKGTIDQIDKTNTYRQTIYVNS 184
DB 322 QTINGQITSTLINEEQTSKELDVKYGKIGINY-ANLNGSIETFNKANRRSHVAFIKPN 380
QY 185 GDNVIAFVLTLGNLKPNTDSNALIDQNTSIRKYK-VDNAADLSESYFVN--PENFEDVT 240
DB 381 NGKTSVTVTGLTMKGSNQG---NQPKRIFEXLGNNEDIKSVYANTTDTSKFKEVT 436
QY 241 NSV--NITFPNPNQYKVEFNTDQITTPYIVVNGHIDPNSKGDALRSTLYGYSNII 298
DB 437 SNMSGNINLQNGSYSINI---ENLDKTYVHYDGEY-LNGTDEVDFRTQVGHPEQLY 491
QY 299 -----WRSMWDNEVAFNNGSGSGDIDKPVV 325
DB 492 KYYYDRGYTLTWDNGLVLYSNKANGENKGPPI 524

RESULT 8

US-09-200-650E-7
; Sequence 7, Application US/09200650E
; Patent No. 6680195
; GENERAL INFORMATION:
; APPLICANT: Patti, Joseph M.
; APPLICANT: Foster, Timothy J.
; APPLICANT: Hook, Magnus A.O.
; APPLICANT: Eidiham, Deirdre Ni
; APPLICANT: Perkins, Samuel L.
; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus
; FILE REFERENCE: P06283US2/BAS
; CURRENT APPLICATION NUMBER: US/09/200,650E
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,815
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/098,427
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-200-650E-7

Query Match 18.7%; Score 323.5; DB 4; Length 1166;
Best Local Similarity 31.2%; Pred. No. 2.4e-19;
Matches 111; Conservative 53; Mismatches 137; Indels 55; Gaps 18;

QY 2 VAADAPAGTDTINQLTNVT-----VGIDSGTTVPYHQAGYKLNFGFVSPNSAVKGDITF 56
DB 269 VAQPAVASNNV-NDLIKVTQKTIKVGDKDNVAAAHDKDIEYDTEFTIDNKVKKGDTM 327
QY 57 KI-----TVPKELNNGVTSTAKVPPIMAGD---QVLANGVID-SDGNVITYFTDYVNTK 107
DB 328 TINYDKNVI PSDL-----TDKNDPIDITDPSGEVIAKGFDPKATKOIYTFFTDYVDKY 380

QY 108 DDVKATLTMFAYIDPENV--KKTGNVTLATGIGSTTANKTVLVYDEKYGKFYNLSIKGTI 165
DB 381 EDIKSRLTLYSYIDKTVPNETSINLTFATAGKETSQN--VTVDYQDBMVHGDNSNIQISIF 438
QY 166 DQIDKTNTYRQTIYVNP---SGDNVIAFVL-----TGNLKPNTDSNALIDQNTSIRK 216
DB 439 TKLDEDQKTI EQCIYVNPFLKKSATNTKVDIAGSQVDYDGNIKLGNGS-TIID-QNTEIKV 496

QY 217 KYVDNAADLSESYFV-NPENFEDVTNSVNTFPNPNQYKVEFNTPD-DQITTPYIVVNG 274
DB 497 YKVNSDQQLPQSNRIYDPSQYEDVTSQ---FDNKKSFSNNVATLDFGDISAYIIKIVS 552
QY 275 HIDEPSKGD-----ALRST-LYGYNSNITWRSMWDNEVAFNNGSGSGDIDKP 323

APPLICANT: Eidlum, Deirdre N.
APPLICANT: Perkins, Samuel L.
TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus
FILE REFERENCE: P06283US2/BAS
CURRENT APPLICATION NUMBER: US/09/200,650E
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,815
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: 60/098,427
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1315
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-200-650E-5

Query Match 14.9%; Score 257.5; DB 4; Length 1315;
Best Local Similarity 26.9%; Pred. No. 1.5e-13;
Matches 88; Conservative 51; Mismatches 157; Indels 31; Gaps 12;

QY 13 ITNQLNTVTVGIDSGTTVPHQAGYKLNFGSPNSAVKGDTEKITVPKELNLNGVT-- 70
DB 251 ITSNTLTIVVDADKNNKIVPAQ-DYLSIKSQITVDKVKSGDYFTIKYSDTVQVGLNDE 309
QY 71 -----STAKVPPIMAGDQVLANGVIDSDGNVI-YTFTDYVNTKDDYKATLTMPAYIDPEN 124
DB 310 DIKNIGDIKP--NNGETIATAKHDITANNLITYTFTDYVDRENSVQMGINSIYMDADT 366
QY 125 VKKTGN-VTLATIGSTTANKTVLVDEKYGKFNLSIKG---TIDQIDKTNT--YRQ 177
DB 367 IPVSKNDVEFNVTIGNTTKTITANIQYPDYVNEKNSIGSAFTETVSHVGNKENPGYXKQ 426
QY 178 TIYVNPSSGDNVIAPVLTGNLKPNTDSNAL-IDQNTSIKVKYVDNAADLSESYFVNPNEN 235
DB 427 TIYVNPSENSTNAKLKVQAYHSSYPNIGQINKDVTDIKIYQVPGYTLNKGYDVNTKE 486
QY 236 FEDVTNSV--NITFPNPQYKVEFNTPPDQITTPYIVVNGHID-PNSKGLALRSTLYG 292
DB 487 LTDVTNQLQKITTYGDNNSAVIDFGNAD-----SAYVMVNTKFOYTNSSEPTLVQMATLS 542
QY 293 YNSNIWRSMWDNEVAFNNSGSGDG 319
DB 543 STGN--KSVSTGNALGFTNNSGAG 566

RESULT 12
US-09-200-650E-3
Sequence 3, Application US/09200650E
Patent No. 6680195
GENERAL INFORMATION:
APPLICANT: Patti, Joseph M.
APPLICANT: Foster, Timothy J.
APPLICANT: Hook, Magnus A.O.
APPLICANT: Eidlum, Deirdre N.
APPLICANT: Perkins, Samuel L.
TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus
FILE REFERENCE: P06283US2/BAS
CURRENT APPLICATION NUMBER: US/09/200,650E
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,815
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: 60/098,427
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 930
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-200-650E-3

Query Match 12.2%; Score 210.5; DB 4; Length 930;
Best Local Similarity 23.1%; Pred. No. 1.1e-09;
Matches 83; Conservative 57; Mismatches 136; Indels 83; Gaps 16;

QY 6 APAAGTDTNQL--TNVTVGIDSG-----TTVPHQAGYKLNFGSPNSAVKGD 55
DB 178 APQGTNVNDKVFHSNIDIAIDKGVNQTTGKTEFWATSSDVLKLIKANYTIDSVKEGDT 237
QY 56 FKITVPKELNLNGVTSTAKVPPIM-AGDQVLANGVIDSDGN-VIYFTDYVNTKDDYKAT 113
DB 238 FTFKYGQYFRPGSVRLPSQTONLYNAQNIIAKGIYDSTNTTYYFTTNVYDQYTNVRS 297
QY 114 LTMPAYIDPEN--VKKTG--NYTLATIGSTTANKTVLVDEKYGKFNLSIKGTIDQI 168
DB 298 FEQVAFAKRKNATTDKTAYKMEVTL-----GNDTYSSEIYDYG-----NKAQPLISST 347
QY 169 DKTNN--TYRQTIYVNPSSGDNVIAPVLTGNL-----KPNTDSNALIDQNTSIKVKYVD 220
DB 348 NYINNEDELGRNMTAYVNQPKNTYTKQTFVTNLTGYKFNPN-----KNFKIYEVT 397
QY 221 NAADLSESYFVNPNFEDVTNSVNTFPNP-----QYKV-EFNTPPDQ 263
DB 398 DQNFVDSFTPDTSKLKDVTDQFDVYISNDNKATATVDLMKQQTSSNKQYIIQVAYPDNS 457
QY 264 ITTPYIVVNGHIDPNSKGLALRSTLYGYSNIIWRSMWDNEVAFNNSGSGGDIDK 322
DB 458 STD-----NKIDYTLDTD---KTKY-----SWSNSYSNVNGSSTANGDQK 495

RESULT 13
US-08-714-402-2
Sequence 2, Application US/08714402
Patent No. 5910441
GENERAL INFORMATION:
APPLICANT: ROCHA, Claudia
APPLICANT: FISCHETTI, Vincent A.
TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN BINDING
TITLE OF INVENTION: PROTEIN FROM GROUP A STREPTOCOCCI
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,402
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 016921-097
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-714-402-2

Query Match 11.8%; Score 204; DB 2; Length 1112;
Best Local Similarity 22.8%; Pred. No. 5.4e-09;

Matches 86; Conservative 72; Mismatches 145; Indels 74; Gaps 18;

QY 8 AAGTDITN--QLTNVTVGIDS--GTT-----VYPHQAQYVKLNFGSVPNASAV---K 52

Db 142 AGSKDVSSSLQLENPKMSVSKYKTEVSSGADFYRNHAAYFKMSFELKQDKSETINP 201

QY 53 GDTFKITVPKELNLTNGVSTAKVPPIM--AGDQVLANGVIDSDGN-VIYFTDYVNTKDD 109

Db 202 GDTFVLQDLRLNPKGISQ--DIPKIYDSANSPLAIGKYHAENHQLIYFTDYIAGLDK 259

QY 110 VKATLTMPAYIDPE-----NVKKT-----GNVTLATGIGSTANKTVLVVYE 151

Db 260 VQLSAELSLFLENKEVLENTSISNPKSTIGGQETIKGTNVVLVGNESTKESNYITNGLS 319

QY 152 KYGKFPYNLSIKGTIDQIDKTNNTYRQTIYVNPSCDNVIAVLTGNL---KPNDSNALI 207

Db 320 NVG-----GSIESYNTETGEFVWVYVNPRTNI--PYATMNLWGFGRARSNTSDLE 369

QY 208 DQONT-----IKYKVDNADLSESYFVNPNF---EDVTNSVNITFPNNOYKVEFN 258

Db 370 NDANTSSAELGEIQVEVEPEGEKLPSSYGVDVTKLTLTDTAGLNGFQMTKRQRIDFG 429

QY 259 TPDDQITTPYIVVNGHIDPNSKGLALRSTLYGNS-----NIWRSMWDNEVAFN 311

Db 430 --NNIQNKAFIIKVTGKTDSGK-PLVVQSNLASFRGASEYAAFTPVGNYVFQNEIALS 486

QY 312 NGSQSGDG--IDKPVV 325

Db 487 PSKSGSGKSEFTKPSI 503

RESULT 14

US-09-327-536-2

; Sequence 2, Application US/09327536

; Patent No. 6355477

; GENERAL INFORMATION:

; APPLICANT: FISCHETTI, Vincent A.

; APPLICANT: ROCHA, Claudia

; TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN BINDING PROTEIN FROM GROUP A

; TITLE OF INVENTION: STREPTOCOCCI

; FILE REFERENCE: 022927-008

; CURRENT APPLICATION NUMBER: US/09/327,536

; CURRENT FILING DATE: 1999-06-08

; PRIOR APPLICATION NUMBER: US 08/714,402

; PRIOR FILING DATE: 1996-09-16

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 1161

; TYPE: PRT

; ORGANISM: SFFBP gene

; US-09-327-536-2

Query Match 11.8%; Score 204; DB 4; Length 1161;

Best Local Similarity 22.8%; Pred. No. 5.7e-09;

Matches 86; Conservative 72; Mismatches 145; Indels 74; Gaps 18;

QY 8 AAGTDITN--QLTNVTVGIDS--GTT-----VYPHQAQYVKLNFGSVPNASAV---K 52

Db 142 AGSKDVSSSLQLENPKMSVSKYKTEVSSGADFYRNHAAYFKMSFELKQDKSETINP 201

QY 53 GDTFKITVPKELNLTNGVSTAKVPPIM--AGDQVLANGVIDSDGN-VIYFTDYVNTKDD 109

Db 202 GDTFVLQDLRLNPKGISQ--DIPKIYDSANSPLAIGKYHAENHQLIYFTDYIAGLDK 259

QY 110 VKATLTMPAYIDPE-----NVKKT-----GNVTLATGIGSTANKTVLVVYE 151

Db 260 VQLSAELSLFLENKEVLENTSISNPKSTIGGQETIKGTNVVLVGNESTKESNYITNGLS 319

QY 152 KYGKFPYNLSIKGTIDQIDKTNNTYRQTIYVNPSCDNVIAVLTGNL---KPNDSNALI 207

Db 320 NVG-----GSIESYNTETGEFVWVYVNPRTNI--PYATMNLWGFGRARSNTSDLE 369

QY 208 DQONT-----IKYKVDNADLSESYFVNPNF---EDVTNSVNITFPNNOYKVEFN 258

Db 370 NDANTSSAELGEIQVEVEPEGEKLPSSYGVDVTKLTLTDTAGLNGFQMTKRQRIDFG 429

QY 259 TPDDQITTPYIVVNGHIDPNSKGLALRSTLYGNS-----NIWRSMWDNEVAFN 311

Db 430 --NNIQNKAFIIKVTGKTDSGK-PLVVQSNLASFRGASEYAAFTPVGNYVFQNEIALS 486

QY 312 NGSQSGDG--IDKPVV 325

Db 487 PSKSGSGKSEFTKPSI 503

RESULT 15

US-09-386-962C-4

; Sequence 4, Application US/09386962C

; Patent No. 6635473

; GENERAL INFORMATION:

; APPLICANT: FOSTER, Timothy

; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCUS

; FILE REFERENCE: P06335US2/BAS

; CURRENT APPLICATION NUMBER: US/09/386,962C

; CURRENT FILING DATE: 1999-08-31

; PRIOR APPLICATION NUMBER: 60/098,443

; PRIOR FILING DATE: 1998-08-31

; PRIOR APPLICATION NUMBER: 60/117,119

; PRIOR FILING DATE: 1999-01-25

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 1742

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

; US-09-386-962C-4

Query Match 11.6%; Score 201.5; DB 4; Length 1742;

Best Local Similarity 21.8%; Pred. No. 1.7e-08;

Matches 79; Conservative 59; Mismatches 146; Indels 79; Gaps 15;

QY 1 MVAADAPAACTDITN--QLTNVTVGID-----SGTIYYPHQAQYVKLNFGSVPNASAVK 53

Db 364 MSLAEPNSGKVNDRKKTINPTLSLNKSNHANNVWPTSNQFNLKANYELDSIKEG 423

QY 54 DTFKITVPKELNLTNGVSTAKVPPIMAGD-QVLANGVIDSDGN-VIYFTDYVNTKDDV 111

Db 424 DFTTIKYGQYIRPGLELPAIKTQLRSKDSIVANGVYDKTNTTFTTYFTNYVDQYNIT 483

QY 112 ATLTPAYIDPEN-VKKTGNVTLATGIGSTTANKTVLVVYEKYGKFPYNLSIKGTIDQIDK 170

Db 484 GSFLLATPKRETAIKDNQNPMEVTIANEVKKDFIYD---YGNKKDNTTAAVAVNDN 540

QY 171 TNNITVRQTIYVNPSCDN-----VIAVLTGNLKP-----TDSNALIDQONTSIKYK 218

Db 541 VNNKHNVEVYILQNNQNPKYAKYFSTVKNGEFIPGEVXYEVTDTNAMVDSFNPDL----- 596

QY 219 VDNAADLSESYFVNPNFEDVTNS-----VNITF-----PNPNQYKVEFNTPDDQ 263

Db 597 -----NSSNVKDVTSQFAPKVSADGTRVDINFAARMANGKTY----- 633

QY 264 ITTPYIVVNGHIDPNSKGLALRSTLY---GYSNIIWRSMWDNEVAFNNGSGSGGIGI 320

Db 634 -----IYQAVRPTGTGNVYTEYWLTRDGTNTNDFYRGTK-STVTYLLNGSSITAGQ- 684

QY 321 DKP 323

Db 685 DNP 687

Search completed: March 26, 2004, 05:10:48

Job time : 78.6259 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 05:00:12 ; Search time 12.6578 Seconds
(without alignments)
493.509 Million cell updates/sec

Title: US-10-056-052A-20
Perfect score: 647
Sequence: 1 QVQLKESGPGLVKPSGTLSTI.....YYGYDGFVYWGQTLTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	78.2	119	1 US-07-634-278-60	Sequence 60, Appl
2	506	78.2	119	1 US-08-477-728-60	Sequence 60, Appl
3	506	78.2	119	1 US-08-474-040-60	Sequence 60, Appl
4	506	78.2	119	1 US-08-487-200-60	Sequence 60, Appl
5	506	78.2	119	3 US-08-484-537-60	Sequence 60, Appl
6	506	78.2	138	1 US-07-634-278-33	Sequence 33, Appl
7	506	78.2	138	1 US-08-477-728-33	Sequence 33, Appl
8	506	78.2	138	1 US-08-474-040-33	Sequence 33, Appl
9	506	78.2	138	1 US-08-487-200-33	Sequence 33, Appl
10	506	78.2	138	3 US-08-484-537-33	Sequence 33, Appl
11	502	77.6	113	2 US-08-606-293-6	Sequence 6, Appl
12	494.5	76.4	137	2 US-08-621-751A-8	Sequence 8, Appl
13	492	76.0	119	2 US-08-752-844-16	Sequence 16, Appl
14	492	76.0	119	2 US-08-591-196-16	Sequence 16, Appl
15	492	76.0	119	4 US-09-293-533-16	Sequence 16, Appl
16	491.5	76.0	242	6 5455030-15	Patent No. 5455030
17	487.5	75.3	120	2 US-08-652-558-8	Sequence 8, Appl
18	487.5	75.3	120	3 US-09-254-189-5	Sequence 5, Appl
19	487.5	75.3	239	2 US-08-860-174A-2	Sequence 2, Appl
20	487	75.3	113	2 US-08-606-293-2	Sequence 2, Appl
21	486.5	75.2	120	2 US-08-652-558-38	Sequence 38, Appl
22	486	75.1	222	2 US-08-190-199A-67	Sequence 67, Appl
23	486	75.1	235	2 US-08-190-199A-61	Sequence 61, Appl
24	481.5	74.4	137	2 US-08-621-751A-4	Sequence 4, Appl
25	479.5	74.1	120	2 US-08-652-558-7	Sequence 7, Appl
26	479.5	74.1	120	3 US-09-254-189-4	Sequence 4, Appl
27	475.5	73.5	241	4 US-09-554-765-13	Sequence 13, Appl

28	471.5	72.9	116	3 US-08-397-411-3	Sequence 3, Appl
29	471.5	72.9	121	3 US-08-881-037-67	Sequence 67, Appl
30	471.5	72.9	273	3 US-08-397-411-6	Sequence 6, Appl
31	471.5	72.9	446	3 US-08-397-411-7	Sequence 7, Appl
32	468	72.3	116	2 US-08-308-494A-21	Sequence 21, Appl
33	467	72.2	119	1 US-08-667-769A-15	Sequence 15, Appl
34	467	72.2	119	1 US-08-667-769A-62	Sequence 62, Appl
35	467	72.2	119	5 PCT-US95-17082A-15	Sequence 15, Appl
36	467	72.2	119	5 PCT-US95-17082A-62	Sequence 62, Appl
37	466.5	72.1	120	2 US-08-652-558-4	Sequence 4, Appl
38	466.5	72.1	120	2 US-08-652-558-5	Sequence 5, Appl
39	466.5	72.1	120	3 US-09-254-189-2	Sequence 2, Appl
40	466.5	72.1	140	3 US-08-943-136-4	Sequence 4, Appl
41	466.5	72.1	140	4 US-08-973-518-4	Sequence 4, Appl
42	465.5	71.9	239	6 5455030-13	Patent No. 5455030
43	464.5	71.8	120	2 US-08-652-558-6	Sequence 6, Appl
44	464.5	71.8	120	3 US-09-254-189-3	Sequence 3, Appl
45	463	71.6	119	1 US-08-467-420A-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-07-634-278-60
Sequence 60, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-60

Query Match 78.2%; Score 506; DB 1; Length 119;
Best Local Similarity 75.2%; Pred. No. 7.4e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGGLVPSQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGMIWGNTDYN 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 QVQLKSGGGLVQPSQSLSTCTVSGFSVTSYGVHWIRQSPGKLEWLGVIWGGSTDYN 60

DB 61 SALKSRLSISKDNSKNQVFLKNSLTADTAVYYCARKGEFYGYDGFVYWGQGLTVTS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 AAFISRLTISKDNSKQVFFKVNSLQPADTAIYYCARAGD--YNYDGFAYWGQGLTVTS 118

QY 121 S 121
DB 119 A 119

RESULT 2
US-08-477-728-60
Sequence 60, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-477-728-60

Query Match 78.2%; Score 506; DB 1; Length 119;
Best Local Similarity 75.2%; Pred. No. 7.4e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGGLVPSQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGMIWGNTDYN 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 QVQLKSGGGLVQPSQSLSTCTVSGFSVTSYGVHWIRQSPGKLEWLGVIWGGSTDYN 60

DB 61 SALKSRLSISKDNSKNQVFLKNSLTADTAVYYCARKGEFYGYDGFVYWGQGLTVTS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 AAFISRLTISKDNSKQVFFKVNSLQPADTAIYYCARAGD--YNYDGFAYWGQGLTVTS 118

QY 121 S 121
DB 119 A 119

RESULT 3
US-08-474-040-60
Sequence 60, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-474-040-60

Query Match 78.2%; Score 506; DB 1; Length 119;
Best Local Similarity 75.2%; Pred. No. 7.4e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDYN 60
Db 1 QVQLKQSGPGLVQPSQSLSTCTVSGFSVTSYGVHWIRQSPGKLEWLGVIWGGSTIDYN 60
QY 61 SALKSRLLSKDSSKNQVFLKMSLTADTAIVYCARKGEEFYGYDGFVYWGQTLVTVS 120
Db 61 AAFISRLTISKDSSKSKQVFEKVNLSLPADTAIYCARAGD--YNYDGFAYWGQTLVTVS 118
QY 121 S 121
Db 119 A 119

RESULT 4

US-08-487-200-60
Sequence 60, Application US/08487200
Patent No. 5693762

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-487-200-60

Query Match 78.2%; Score 506; DB 1; Length 119;
Best Local Similarity 75.2%; Pred. No. 7.4e-44;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDYN 60
Db 1 QVQLKQSGPGLVQPSQSLSTCTVSGFSVTSYGVHWIRQSPGKLEWLGVIWGGSTIDYN 60
QY 61 SALKSRLLSKDSSKNQVFLKMSLTADTAIVYCARKGEEFYGYDGFVYWGQTLVTVS 120
Db 61 AAFISRLTISKDSSKSKQVFEKVNLSLPADTAIYCARAGD--YNYDGFAYWGQTLVTVS 118
QY 121 S 121
Db 119 A 119

RESULT 5

US-08-484-537-60
Sequence 60, Application US/08484537
Patent No. 6180370

GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

QY 1 QVOLKESGPGIVKPSQTLSTCTTSGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDYN 60
 Db 20 QVOLKQSGPGIVQPSQSLSTCTVSGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDYN 79
 QY 61 SALKSRSLSKDNGSKNQVFLKMSLTADTAIVYCCARKGEFFYYGYDGFVYWGQGLTVTS 120
 Db 80 AAFISRLTISKDNGSKNQVFLKMSLTADTAIVYCCARKGEFFYYGYDGFVYWGQGLTVTS 137
 QY 121 S 121
 Db 138 A 138

RESULT 8

US-08-474-040-33
 ; Sequence 33, Application US/08474040
 ; Patent No. 5693761

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
 APPLICANT: CO, Man Sung
 APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas F.
 APPLICANT: COELINGH, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,040
 FILING DATE: 07-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/634,278
 FILING DATE: 19-DEC-1990
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:
 LENGTH: 138 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-474-040-33

Query Match 78.2%; Score 506; DB 1; Length 138;
 Best Local Similarity 75.2%; Pred. No. 8.8e-44;
 Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVOLKESGPGIVKPSQTLSTCTTSGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDYN 60
 Db 20 QVOLKQSGPGIVQPSQSLSTCTVSGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDYN 79
 QY 61 SALKSRSLSKDNGSKNQVFLKMSLTADTAIVYCCARKGEFFYYGYDGFVYWGQGLTVTS 120
 Db 80 AAFISRLTISKDNGSKNQVFLKMSLTADTAIVYCCARKGEFFYYGYDGFVYWGQGLTVTS 137
 QY 121 S 121
 Db 138 A 138

RESULT 9

US-08-487-200-33
 ; Sequence 33, Application US/08487200
 ; Patent No. 5693762

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
 APPLICANT: CO, Man Sung
 APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas F.
 APPLICANT: COELINGH, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,200
 FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/634,278
 FILING DATE: 19-DEC-1990
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:
 LENGTH: 138 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-487-200-33

Query Match 78.2%; Score 506; DB 1; Length 138;
 Best Local Similarity 75.2%; Pred. No. 8.8e-44;
 Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

Qy	1	QVQLKESGPGLVKPSQTLSTICTISGFSLSRYSVHWVRQPPGKGLWLGMIWGGENDYN	60
		: : : : : : :	
Db	20	QVQLKSGPGGLVQPSQSLSTICTVSGFSVTSYGVHWIRQSPGKLEWLGVIMSGSTIDYN	79
Qy	61	SALKSRSLISKDNSKNQVFLKMNSLTAADTAVVYCARKEGFYYGYDGFVYMGQGLTVS	120
		: : : : : : :	
Db	80	AAFLISLTLISKDNSKQVFFKVNSLQPADTAIYYCARAGD--YNYDGFAYMGQGLTVS	137
Qy	121	S	121
		:	
Db	138	A	138

RESULT 10

```

: Sequence 33, Application US/08484537
: Patent No. 6180370
: GENERAL INFORMATION:
: APPLICANT: QUEEN, Cary L.
: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOUFI, Nicholas F.
: APPLICANT: COELINGH, Kathleen L.
: APPLICANT: SELICK, Harold E.
: TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Khourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,537
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/634,278
: FILING DATE: 19-DEC-1990
: APPLICATION NUMBER: US 07/590,274
: FILING DATE: 28-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/310,252
: FILING DATE: 13-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/290,975
: FILING DATE: 28-DEC-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-002600
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 138 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-484-537-33

```

Query Match	78.2%;	Score 506;	DB 3;	Length 138;
Best Local Similarity	75.2%;	Pred. No. 8.8e-44;		
Matches	91;	Conservative	16;	Mismatches 12;
				Indels 2;
				Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSITCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGNTDYN 60

[illegible]

RESULT 11

US-08-606-293-6
Sequence 6, Application US/08606293
Patent No. 5874082
GENERAL INFORMATION:
APPLICANT: de Boer, Mark
TITLE OF INVENTION: Humanized Anti-CD40 Monoclonal Antibodies and
TITLE OF INVENTION: Fragments Capable of Blocking B Cell Activation
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION Intellectual Property - R440
STREET: 4560 Horton Street, P.O. Box 8097
CITY: Emeryville
STATE: California
COUNTRY: United States of America
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,293
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/070,158
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Saveriede, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 27527/33157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-293-6

Query Match	77.6%;	Score 502;	DB 2;	Length 113;
Best Local Similarity	81.0%;	Pred. No. 1.8e-43;		
Matches 98;	Conservative 7;	Mismatches 8;	Indels 8;	Gaps 2.

QY	1 QVQLKESGPGLVKPSQTLSITCTISGFSLSRYSVHWVRQPPGKGLEWLGIMWGNGNTDYN	60
	: : : : :	
	: : : : :	
D8	1 QVQLVESGPGLVKPSSQSLSTCTVSGFSLRSRYSVHWVRQPPGKGLEWLGIMWGNGSSTDYN	60
	: : : : :	
	: : : : :	
QY	61 SALKSRISTSKDNISKNOVFLLKNNSLTADPTAVYYCARKEGFYYGYDGFFVYWGGTLVTVS	120
	: : : : :	
	: : : : :	
D8	61 SALKSRILTISKDTSKNOVFLLKNNSLRADPTAMYYCVRT-----DG-DYWGQGITVTVS	112
	: : : : :	
	: : : : :	

QY	121	S	121
Db	113	S	113


```
RESULT 12
US-08-621-751A-8
; Sequence 8, Application US/08621751A
; Patent No. 5882644
; GENERAL INFORMATION:
; APPLICANT: Chang, Chung N.
; APPLICANT: Landolf, Nicholas F.
; APPLICANT: Martin, Ulrich
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER LLP
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,751A
; FILING DATE: 22-MAR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 321152000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141 MRSN FOERS SFO
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-621-751A-8

Query Match          76.4%; Score 494.5; DB 2; Length 137;
Best Local Similarity 76.9%; Pred. No. 1.3e-42;
Matches 93; Conservative 14; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGCGNTDYN 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQESGPGLVKPSSETLTSLCTVSGFSLTNVAINWVRQPPGKGLEWLGMIWGCGTSYN 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SALKSRLISKDNSKNQVFLKMNSLTAADTAIVYVCARKGEFYGYDGFVYWGQGLVTVS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 SALKSRLITISKDTSKNQVSLKLSVTAADTAIVYVCARTGTGRGYFFD---YWGQGLVTVS 136
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 S 121
Db 137 S 137

RESULT 13
US-08-752-844-16
; Sequence 16, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schief, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-752-844-16

Query Match          76.0%; Score 492; DB 2; Length 119;
Best Local Similarity 78.7%; Pred. No. 1.9e-42;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGCGNTDYN 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLKESGPGLVAPSQSLTCTVSGFSLTSYGVHWVRQPPGKGLEWLGMIWGDSSTNYN 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SALKSRLISKDNSKNQVFLKMNSLTAADTAIVYVCARK-GEFYGYDGFVYWGQGLVTV 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SALKSRLISKDNSKQVFLKMNSLQTDTDARTARYCAREXXXXXXYYAMD---YWGQGSVTV 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 120 SS 121
Db 118 SS 119

RESULT 14
US-08-591-196-16
; Sequence 16, Application US/08591196
; Patent No. 5977316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/591,196
FILING DATE: 16-JAN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-591-196-16

Query Match 76.0%; Score 492; DB 2; Length 119;
Best Local Similarity 78.7%; Pred. No. 1.9e-42;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGNTDYN 60
DB 1 QVQLKESGPGLVAPSQSLSTICTVSGFSLTSYGVHWVRQPPGKLEWLGIMWGDSITNYN 60
QY 61 SALKSRLSISKDNSKNQVFLKNSLTADTAVYYCARK-GEFYGYDGFVYWGQITLVTV 119
DB 61 SALKSRLSISKDNSKQVFLKNSLTQDDTARYYCAREXXXXYYAMD---YWGQISVTYV 117
QY 120 SS 121
DB 118 SS 119

RESULT 15
US-09-293-533-16
Sequence 16, Application US/09293533
Patent No. 6509016
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Poon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,533
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-293-533-16

Query Match 76.0%; Score 492; DB 4; Length 119;
Best Local Similarity 78.7%; Pred. No. 1.9e-42;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGNTDYN 60
DB 1 QVQLKESGPGLVAPSQSLSTICTVSGFSLTSYGVHWVRQPPGKLEWLGIMWGDSITNYN 60
QY 61 SALKSRLSISKDNSKNQVFLKNSLTADTAVYYCARK-GEFYGYDGFVYWGQITLVTV 119
DB 61 SALKSRLSISKDNSKQVFLKNSLTQDDTARYYCAREXXXXYYAMD---YWGQISVTYV 117
QY 120 SS 121
DB 118 SS 119

Search completed: March 26, 2004, 05:11:57
Job time : 51.6578 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2004, 05:07:57 ; Search time 381.665 Seconds
(without alignments)
82.955 Million cell updates/sec

Title: US-10-056-052A-20
Perfect score: 647
Sequence: 1 QVQLKESGPGLVKPSQTLSTI.....YYGYDGFVYWGQTLVTSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647	100.0	121	14	US-10-056-052-20 Sequence 20, Appl
2	605	93.5	121	14	US-10-056-052-12 Sequence 12, Appl
3	538.5	83.2	118	14	US-10-056-052-16 Sequence 16, Appl
4	524.5	81.1	118	14	US-10-056-052-8 Sequence 8, Appl
5	506	78.2	119	12	US-10-389-417-19 Sequence 19, Appl
6	506	78.2	119	15	US-10-389-155-19 Sequence 19, Appl
7	506	78.2	138	12	US-10-389-417-46 Sequence 46, Appl
8	506	78.2	138	15	US-10-389-155-46 Sequence 46, Appl
9	496	76.7	121	12	US-09-842-776A-52 Sequence 52, Appl
10	493	76.2	121	14	US-10-207-655-252 Sequence 252, App
11	493	76.2	271	14	US-10-207-655-254 Sequence 254, App
12	493	76.2	556	14	US-10-207-655-268 Sequence 268, App
13	492	76.0	119	12	US-10-239-656-23 Sequence 23, Appl
14	492	76.0	119	14	US-10-153-401-16 Sequence 16, Appl
15	491.5	76.0	119	13	US-10-140-555-2 Sequence 2, Appl

16	487.5	75.3	116	14	US-10-169-351-108	Sequence 108, App
17	487	75.3	138	15	US-10-374-531-8	Sequence 8, Appl
18	487	75.3	138	15	US-10-374-531-13	Sequence 13, Appl
19	484.5	74.9	116	14	US-10-194-975-100	Sequence 100, App
20	476	73.6	119	14	US-10-232-187-2	Sequence 2, Appl
21	475.5	73.5	241	16	US-10-353-721-13	Sequence 13, Appl
22	474.5	73.3	139	8	US-08-779-784-37	Sequence 37, Appl
23	472.5	73.0	120	14	US-10-194-975-112	Sequence 112, App
24	471.5	72.9	116	12	US-10-435-299-3	Sequence 3, Appl
25	471.5	72.9	273	12	US-10-435-299-6	Sequence 6, Appl
26	471.5	72.9	333	14	US-10-059-261-61	Sequence 61, Appl
27	471.5	72.9	446	12	US-10-435-299-7	Sequence 7, Appl
28	471.5	72.9	972	15	US-10-418-836-38	Sequence 38, Appl
29	471.5	72.9	975	15	US-10-418-836-39	Sequence 39, Appl
30	469.5	72.6	120	12	US-10-239-656-33	Sequence 33, Appl
31	469.5	72.6	120	12	US-10-239-656-43	Sequence 43, Appl
32	469.5	72.6	510	12	US-10-239-656-48	Sequence 48, Appl
33	469.5	72.6	510	12	US-10-239-656-49	Sequence 49, Appl
34	469	72.5	253	12	US-10-239-656-63	Sequence 63, Appl
35	468.5	72.4	139	9	US-09-881-823-4	Sequence 4, Appl
36	468.5	72.4	250	14	US-10-194-975-110	Sequence 110, App
37	467	72.2	119	14	US-10-144-644-15	Sequence 15, Appl
38	467	72.2	119	14	US-10-144-644-62	Sequence 62, Appl
39	466.5	72.1	135	8	US-08-779-784-32	Sequence 32, Appl
40	466.5	72.1	140	9	US-09-007-093-4	Sequence 4, Appl
41	466.5	72.1	140	15	US-10-428-754-4	Sequence 4, Appl
42	465.5	71.9	135	15	US-10-010-729-68	Sequence 68, Appl
43	465	71.9	117	15	US-10-371-797-11	Sequence 11, Appl
44	464.5	71.8	122	14	US-10-207-655-360	Sequence 360, App
45	464.5	71.8	141	14	US-10-207-655-359	Sequence 359, App

ALIGNMENTS

RESULT 1
US-10-056-052-20
; Sequence 20, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30.
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-056-052-20

Query Match 100.0%; Score 647; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 9e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLKESGPGLVKPSQTLSTICTISGFSLSRYSVHWVRQDPFGKGLWLGIMWGNTDYN 60
DB 1 QVQLKESGPGLVKPSQTLSTICTISGFSLSRYSVHWVRQDPFGKGLWLGIMWGNTDYN 60

[illegible]

```

RESULT 2
US-10-056-052-12
; Sequence 12, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALP, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLEA PROTEIN . . .
; FILE REFERENCE: P07063US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056, 052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308, 116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298, 413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274, 611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264, 072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-12

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Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
93.5%;	92.6%;	605;	14;	121;	4;	5;	0;
Matches	112;	Conservative					
QY	1	QVQLKESGPGLVKPSQTLSTICTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGNTDYN	60				
Db	1	QVQLKESGPGLVAPSQSLSTICTAISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGNTDYN	60				
QY	61	SALKSRPLSISKDNSKNQVFLKONSLTAADTAVVYCARKGEEFYGYDGFVYWGGTLVTVS	120				
Db	61	SALKSRPLSISKDNSKSQVFLKONSLQTDTDATVYCARKGEEFYGYDGFVYWGGTLVTVS	120				
QY	121	S	121				
Db	121	A	121				

RESULT 3
US-10-056-052-16
Sequence 16, Application US/10056052
Publication No. US2003009656A1
GENERAL INFORMATION:
APPLICANT: PATTI, Joseph M
APPLICANT: HUTCHINS, Jeff T
APPLICANT: DOMANSKI, Paul
APPLICANT: PATEL, Pratiksha
APPLICANT: HALL, Andrea
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
FILE REFERENCE: P07069US04/BAS
CURRENT APPLICATION NUMBER: US/10/056,052
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/308,116
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/298,413

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; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 118
; TYPE: prt
; ORGANISM: Staphylococcus aureus
US-10-056-052-16

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Query Match	83.2%;	Score 538.5;	DB 14;	Length 118;
Best Local Similarity	84.3%;	Pred. NO. 3.7e-45;		
Matches 102;	Conservative	6;	Mismatches 10;	Indels 3;
				Gaps 1;

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QY      1 QVQLKESGPGLVKPSQTLTCTISGFSLSRYSVHWVROPFGKGLEWLGMIWGGENTDYN 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 QVQLKESGPGLVAPSQSLTCTVSGFSLSRYSVHWVROPFGKGLEWLGMIWGGENTDYN 60
QY      61 SAKSRSLTISKDNSKNQVFLKNSLTAADTAVYYCARKEGFYYGYDGFVYWGQGLTVTS 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 SAKSRSLTISKDNSKQVFLKNSLQTDLTAVYYCATA--YYGNSMFAFWGQGLTVTS 117
QY      121 S 121
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Db      118 A 118
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```

RESULT 4
US-10-056-052-8
; Sequence 8, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
; FILE REFERENCE: P07063US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056, 052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308, 116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298, 413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274, 611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264, 072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-8

```

```

Query Match      81.1%; Score 524.5; DB 14; Length 118;
Best Local Similarity 81.8%; Pred. No. 8.7e-44;
Matches 99; Conservative 7; Mismatches 12; Indels 3; Gaps 1.

```

Db 118 A 118

RESULT 5

US-10-389-417-19

Sequence 19, Application US/10389417

Publication No. US20040049014A1

GENERAL INFORMATION:

APPLICANT: Queen, Cary L.

Co, Man Sung

Schneider, William P.

Landolfi, Nicholas F.

Coelingh, Kathleen L.

Selick, Harold E.

TITLE OF INVENTION: Improved Humanized Immunoglobulins

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/389,417

FILING DATE: 13-Mar-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000

FILING DATE: 01-JUN-1999

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 08/484,537

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 011823-002650US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-389-417-19

Query Match 78.2%; Score 506; DB 12; Length 119;

Best Local Similarity 75.2%; Pred.No. 5.7e-42;

Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTICTGISGFSLSRYSVHWYRQPPGKLEWLGIMWGQNTDYN 60

Db 1 QVQLKQSGPGLVQPSQSLITCTVSGFSVTSTYGVHWIRQSPGKLEWLGIVWGGSTDYN 60

QY 61 SALKSRLLSKDNSKQVFLKNSLTADTAVVYCARGEFFYYGYDGFVYWGQTLTVTS 120

Db 61 AAFISRLTISKDNSKQVFFKYNLSIQPADTAIYYCARAGD--YNYDGFAYWGQTLTVTS 118

QY 121 S 121

Db 119 A 119

RESULT 6

US-10-389-155-19

Sequence 19, Application US/10389155

Publication No. US20030229208A1

GENERAL INFORMATION:

APPLICANT: Queen, Cary L.

Co, Man Sung

Schneider, William P.

Landolfi, Nicholas F.

Coelingh, Kathleen L.

Selick, Harold E.

TITLE OF INVENTION: Improved Humanized Immunoglobulins

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/389,155

FILING DATE: 13-Mar-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000

FILING DATE: 01-JUN-1999

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 08/484,537

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 011823-002650US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-389-155-19

Query Match 78.2%; Score 506; DB 15; Length 119;

Best Local Similarity 75.2%; Pred.No. 5.7e-42;

Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTICTGISGFSLSRYSVHWYRQPPGKLEWLGIMWGQNTDYN 60

Db 1 QVQLKQSGPGLVQPSQSLITCTVSGFSVTSTYGVHWIRQSPGKLEWLGIVWGGSTDYN 60


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Db 20 QVQLKQSGPGLVQPSSQSLSTCTVSGFSTVSYGVHWIRQSPGKLEMLGVIMSGGSTDYN 79
QY 61 SALKSRSLISKDNSKNQVFLKMSLTAADTAIVYCCARKGEFYGYDGFVYWGQGLTVTVS 120
Db 80 AAFISRLTISKDNSKSKQVFFKVNLSLPADTAIYYCARAGD--YNYDGFAYWGQGLTVTVS 137
QY 121 S 121
Db 138 A 138
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```
RESULT 9
US-09-842-776A-52
; Sequence 52, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-842-776A-52
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Query Match 76.7%; Score 496; DB 12; Length 121;
Best Local Similarity 79.7%; Pred. No. 5.6e-41;
Matches 98; Conservative 8; Mismatches 13; Indels 4; Gaps 3;

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QY 1 QVQ-LKESGPGLVKPSQTLSTCTTISGFSLSRYSVHWVRQPPGKLEMLGMWGGNTDY 59
Db 1 EVQLLESGPGLVAPSSQSLSTCTVSGFSLSRYSVHWVRQPPGKLEMLGMWGGSTDY 60
QY 60 NSALKSRSLISKDNSKNQVFLKMSLTAADTAIVYCCARK-GEFYGYDGFVYWGQGLTVT 118
Db 61 NSGLKSRSLISKDNSKQVFLKMSLQTDITAIYYCARNMGGRRYPDY--FDYWGQGLTVT 118
QY 119 VSS 121
Db 119 VSS 121
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RESULT 10
US-10-207-655-252
; Sequence 252, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 252
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-252
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Query Match 76.2%; Score 493; DB 14; Length 121;
Best Local Similarity 78.5%; Pred. No. 1.1e-40;

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Matches 95; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
QY 1 QVQLKESGPGLVKPSQTLSTCTTISGFSLSRYSVHWVRQPPGKLEMLGMWGGNTDYN 60
Db 1 QVQLKESGPGLVAPSSQSLSTCTVSGFSLTGYVNWVRQPPGKLEMLGMWGDGSTDYN 60
QY 61 SALKSRSLISKDNSKNQVFLKMSLTAADTAIVYCCARKGEFYGYDGFVYWGQGLTVTVS 120
Db 61 SALKSRSLITKDNSKQVFLKMSLQTDITARIYYCARDGYSNFHYVMDYWGQGSTVTVS 120
QY 121 S 121
Db 121 S 121
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```
RESULT 11
US-10-207-655-254
; Sequence 254, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 254
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-254
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Query Match 76.2%; Score 493; DB 14; Length 271;
Best Local Similarity 78.5%; Pred. No. 2.7e-40;
Matches 95; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

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QY 1 QVQLKESGPGLVKPSQTLSTCTTISGFSLSRYSVHWVRQPPGKLEMLGMWGGNTDYN 60
Db 151 QVQLKESGPGLVAPSSQSLSTCTVSGFSLTGYVNWVRQPPGKLEMLGMWGDGSTDYN 210
QY 61 SALKSRSLISKDNSKNQVFLKMSLTAADTAIVYCCARKGEFYGYDGFVYWGQGLTVTVS 120
Db 211 SALKSRSLITKDNSKQVFLKMSLQTDITARIYYCARDGYSNFHYVMDYWGQGSTVTVS 270
QY 121 S 121
Db 271 S 271
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RESULT 12
US-10-207-655-268
; Sequence 268, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 268
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-268
```


; CURRENT APPLICATION NUMBER: US/10/140,555
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/443,790
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/109,041
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-140-555-2

Query Match 76.0%; Score 491.5; DB 13; Length 119;
Best Local Similarity 79.3%; Pred. No. 1.5e-40;
Matches 96; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTICTISGFSLSRYSVHWVRQPPGKLEWLGMIWGQNTDYN 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLKESGPGLVKPSQSLSTICTIVSGFSLTGYNWVRQPPGKLEWLGMIWVDGTDYN 60
QY 61 SALKSRISISKDNSKNQVFLKNSLTADTAVYYCARKGEFYGYDGFVYWGQITVTS 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SALKSRISISKDNSKQVFLKNSLTQDTARYYCARGSSLL--GFAYWGQITVTS 117
QY 121 S 121
Db 118 A 118

Search completed: March 26, 2004, 05:54:12
Job time : 409.665 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:17 ; Search time 12.4433 Seconds
(without alignments)
935.380 Million cell updates/sec

Title: US-10-056-052A-20
Perfect score: 647
Sequence: 1 QVQLKESGPGLVKPSQTLST.....YYGYDGFVYWGQGLVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	534.5	82.6	117	2 S38563	Ig heavy chain V r
2	489	75.6	114	2 S11106	Ig heavy chain V r
3	489	75.6	140	2 S55028	Ig heavy chain V r
4	488	75.4	127	2 B31807	Ig heavy chain V r
5	487.5	75.3	122	2 S20809	Ig heavy chain V r
6	486.5	75.2	139	2 A32456	Ig heavy chain pre
7	482.5	74.6	122	2 A49049	Ig heavy chain V r
8	482	74.5	144	1 G2MS14	Ig heavy chain pre
9	478.5	74.0	135	2 S31913	Ig gamma-2A chain
10	477	73.7	112	2 S11100	Ig heavy chain V r
11	477	73.7	113	2 S11101	Ig heavy chain V r
12	476.5	73.6	115	2 S26470	Ig heavy chain V r
13	472	73.0	116	2 S11102	Ig heavy chain V r
14	470	72.6	140	2 S14238	Ig gamma-1 chain p
15	466.5	72.1	116	2 S42484	Ig heavy chain V r
16	465.5	71.9	141	2 S52446	Ig heavy chain V r
17	465.5	71.9	144	2 S11244	Ig gamma-2a chain
18	465	71.9	121	2 D30560	Ig heavy chain V r
19	464.5	71.8	120	2 PL0087	Ig heavy chain V r
20	464	71.7	114	2 S11099	Ig heavy chain V r
21	463	71.6	111	2 S26324	Ig heavy chain V r
22	459	70.9	115	2 S11103	Ig heavy chain V r
23	457.5	70.7	118	2 S32786	Ig heavy chain (an
24	457	70.6	115	2 S11107	Ig heavy chain V r
25	452	69.9	110	2 S26323	Ig heavy chain V r
26	452	69.9	118	2 PQ0266	Ig heavy chain V r
27	451	69.7	112	2 S11108	Ig heavy chain V r
28	450	69.6	231	2 PC4155	Ig gamma-2b chain
29	448.5	69.3	107	2 S14492	Ig heavy chain V r

30	447.5	69.2	107	2 S14493	Ig heavy chain V r
31	447	69.1	106	2 S26322	Ig heavy chain V r
32	443	68.5	109	2 PH1026	Ig heavy chain V r
33	443	68.5	112	2 S11098	Ig heavy chain V r
34	441.5	68.2	107	2 S14491	Ig heavy chain V r
35	441.5	68.2	110	2 PH1024	Ig heavy chain V r
36	440	68.0	121	2 S33131	Ig heavy chain V r
37	439.5	67.9	106	2 S14489	Ig heavy chain V r
38	437	67.5	117	2 S10111	Ig heavy chain V r
39	435	67.2	116	2 PL0198	anti-DNA autoantib
40	434	67.1	115	1 HVMS14	Ig heavy chain pre
41	433	66.9	109	2 PH1025	Ig heavy chain V r
42	433	66.9	114	2 S26321	Ig heavy chain V r
43	433	66.9	114	2 S11104	Ig heavy chain V r
44	431.5	66.7	107	2 S14506	Ig heavy chain V r
45	428	66.2	114	2 S11105	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S38563.
Ig heavy chain V region (ASW61) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S38563
R/Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A/Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s Mj
A/Reference number: S38559
A/Accession: S38563
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-117 <MON>
A/Cross-references: EMBL:X75099; NID:g414151; PIDN:CAA52990.1; PID:g414152
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 534.5; DB 2; Length 117;
Best Local Similarity 85.0%; Pred. No. 9e-43;
Matches 102; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTICTTISGFSLSRYSVHWVROPPGKGLWLGIMWGQNTDYN 60
DB 1 QVQLKESGPGLVAPSQSLSTICTVSGFSLRSYSVHWVRQPPGKGLWLGIMWGQNTDYN 60
QY 61 SALKSRSLISKDNSKQVFLKNSLTAAADTAVVYCARKEGFYYGYDGFVYWGQTLTVS 120
DB 61 SALKSRSLISKDNSKQVFLKNSLTQDDTAVVYCARDDGYDYDAMD---YWGQTSVTVS 117

RESULT 2
S11106
Ig heavy chain V region (clone NQ5-96.2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C/Accession: S11106
R/Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A/Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone
A/Reference number: S07331; MUID:83271467; PMID:6877353
A/Accession: S11106
A/Molecule type: mRNA
A/Residues: 1-114 <NAT>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 75.6%; Score 489; DB 2; Length 114;
Best Local Similarity 76.9%; Pred. No. 1.5e-38;
Matches 93; Conservative 8; Mismatches 12; Indels 8; Gaps 1;

```
QY      1 QVQLKESGPGLVKPSQ1LSITCTIGSFSLRSYVHWVRQPPGKGL2EWLGMWGGNDYN 60
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db      1 QVQLKESGPGLVKPSQ1LSITCTVSGXSLTSYGVHWVRQPPGKLEWLGVIWAGSTNYN 60
QY      61 SALKSR1LSTISKDN2SKNQVFLK3NSLTAADTAVVYCCARKGEFYGYDGFVYWGQGLTVTS 120
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db      61 SALKSR1LSTISKDN2SKSQVFLK3NSLQ4TD5TAMYYCAR-----DGFAYWGQGSTVTVS 112
QY      121 S 121
      |
Db      113 S 113
```

```

RESULT 3
S55028
Ig heavy chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
C/Accession: S55028
R/Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolies, M.N.; Sheriff
U. Mol. Biol. 248, 344-360, 1995
A/Title: Structure and specificity of the anti-digoxin antibody 40-50.
A/Reference number: S55027; MUID:95257394; PMID:7739045
A/Accession: S55028
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-140 <JEF>
A/Cross-references: EMBL:L31403; NID:g476717; PIDN:AAA38191.1; PID:g476718
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
E/34-116/Domain: immunoglobulin homology <IMM>

```

[illegible]

RESULT 4
B31807
Ig heavy chain V region (PAC1) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 23-May-1997
C/Accession: B31807
R/Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt
J. Biol. Chem. 264, 259-265, 1989
A/Title: A monoclonal antibody against the platelet fibrinogen receptor contains a sequ
A/Reference number: A31807; MUID:89079661; PMID:2909518
A/Accession: B31807
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-127 <TAU>
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F.15-97/Domain: immunoglobulin homology <IMM>

Query Match	75.4%;	Score 488;	DB 2;	Length 127;
Best Local Similarity	72.4%;	Pred. No. 2.1e-38;		
Matches 92;	Conservative 11;	Mismatches 18;	Indels 6;	Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSITCTISGFSLSRYSVHWVRQPPGKGLEWLGIMWGNGNTDYN 60

Db 1 QVQLKQSGEGLVQPSSQSLSTICTVSGFSLTSYGVHWVRISPGKLEMLGVITWSSGSDYN 60

QY 61 SALKSRLEISKDNKSNQVFLKMNSLTAADTAVYYCARKEGFYYGYDG-----FVYWGQG 114
: ||||| ||| : ||| : ||| |||||

Db 61 AAFISRLISKDNKSQVFFKMNSLQANDTGIYYCARRSPSYRYRDGAGPYIAMDYWGQ 120
: ||||| ||| : ||| : ||| |||||

QY 115 TLVTVSS 121
: |||||

Db 121 TSVTVSS 127

RESULT 5
S20809
Ig heavy chain V region (hybridoma C8) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S20809
R/Hoogenboom, H.; Dubois, P.; Raus, J.; Volckaert, G.
submitted to the EMBL Data Library, September 1990
A/Description: Nucleotide sequences of the variable region cDNAs encoding a murine antibody
A/Reference number: S20809
A/Accession: S20809
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-122 <HOO>
A/Cross-references: EMBL:X54692; NID:G50249; PIDN:CA38508.1; PID:G50250
C/Superfamily: immunoglobulin V region, immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

[illegible]

RESULT 6
A32456
Ig heavy chain precursor V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C/Accession: A32456
R/Dombrink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.
J. Biol. Chem. 264, 4513-4522, 1989
A/Title: Variable region primary structures of a high affinity anti-fluorescein immunoglobulin
A/Reference number: A32456; MUID:89174706; PMID:2494173
A/Accession: A32456
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-139 <DOM>
A/Cross-references: GB:J04609; NID:G556316; PIDN:AAA50298.1; PID:G556317
A/Note: the authors translated the codon CAC for residue 20 as Gln, and CAC for residue 21 as Gln
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-116/Domain: immunoglobulin homology <IMM>

Query Match	75.2%;	Score 486.5;	DB 2;	Length 139;
Best Local Similarity	77.0%;	Pred. No. 3.1e-38;		
Matches 94;	Conservative	9;	Mismatches 14;	Indels 5;
				Gaps 2;

QY 2 VQLKESGPGLVKPSQTLSTCTTSGFSLSRYSVHWVROEPGKLEWLGMIWGGNDYNS 61

Db 21 VHLKESGFLVAPSQSLSTCTVSGFSLTNVGVHWVRQPPGKGLEWLGVIWAGNTNYS 80
QY 62 ALKSRLSISKDNSKNQVFLKMNSLTAADTAVVYCARKE--FYYGDPGEFVWGQTLVTV 119
Db 81 ALMSRLSISKDNSKSKQVFLKMNSLQIDDTAIVYCAKRLERIFYAMD---YWGQTSVTV 137
QY 120 SS 121
Db 138 SS 139

RESULT 7
A49049
Ig heavy chain V region (anti-idiotypic) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C/Accession: A49049
R/Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992
A/Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen
A/Reference number: A49049; MUID:93049629; PMID:1425914
A/Accession: A49049
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-122 <ARM>
A/Experimental source: BALB/c
A/Note: sequence extracted from NCBI backbone (NCBIN:118295, NCBIPI:118296)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 482.5; DB 2; Length 122;
Best Local Similarity 76.0%; Pred. No. 6.4e-38;
Matches 92; Conservative 11; Mismatches 15; Indels 3; Gaps 1;
QY 1 QVOLKESGFLVLPSPQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDYN 60
Db 1 QVOLKESGFLVAPSQSLSTCTVSGFSITDYVSWIRQPPGKLEWLGVIWGGNTYYN 60
QY 61 SALKSRLSISKDNSKNQVFLKMNSLTAADTAVVYCARKEFYGYDGFVWGQTLVTVS 120
Db 61 SALKSRLSISKDNSKQVFLKMNSLQDPTAMYYCAKHDEITTFD---YWGQGTTLTVS 117
QY 121 S 121
Db 118 S 118

RESULT 8
G2MS14
Ig heavy chain precursor V region (MOPC 141) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 16-Jun-2000
C/Accession: A02094
R/Sakano, H.; Maki, R.; Kurosawa, Y.; Roeder, W.; Tonegawa, S.
Nature 286, 676-683, 1980
A/Title: Two types of somatic recombination are necessary for the generation of complete
A/Reference number: A93229; MUID:81012133; PMID:6774258
A/Accession: A02094
A/Molecule type: DNA
A/Residues: 1-144 <SAK>
A/Cross-references: GB:V00768; GB:J00491; NID:951615; PIDN:CAA24149.1; PID:951616
A/Note: the sequence shown was determined from a differentiated gene isolated from a myeloma cell line. The authors translated the codon TAT for residue 51 as Thr and TTA for residue 9
C/Genetics:
A/Introns: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-144/Product: Ig heavy chain V region (MOPC 141) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score482; DB 1; Length 144;

Best Local Similarity 74.4%; Pred. No. 8.5e-38;
Matches 93; Conservative 9; Mismatches 19; Indels 4; Gaps 1;
QY 1 QVOLKESGFLVLPSPQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDYN 60
Db 20 QVOLKESGFLVAPSQSLSTCTVSGFSLTGYNWVRQPPGKLEWLGTIWNGSTDYN 79
QY 61 SALKSRLSISKDNSKNQVFLKMNSLTAADTAVVYCARKEFYGYDGFVWGQTL 116
Db 80 STLKSLTITKDNSKSKQVFLKMNSLQDPTARYYCASVSITYYGRSDKYFTLDYWGQTS 139
QY 117 VTSS 121
Db 140 VTSS 144

RESULT 9
S31913
Ig gamma-2A chain precursor - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 23-Jul-1999
C/Accession: S31913
R/Bespalov, I.A.; Hilyanov, P.A.; Lukashovich, L.V.; Lunev, V.E.; Tribush, S.S.; Gaponova, submitted to the EMBL Data Library, January 1993
A/Reference number: S31913
A/Accession: S31913
A/Molecule type: mRNA
A/Residues: 1-135 <BES>
A/Cross-references: EMBL:X70822; NID:957921; PIDN:CAA50153.1; PID:957922
A/Experimental source: strain BALB/c
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;1-11/Domain: signal sequence #status predicted <SIG>
F;12-135/Product: Ig gamma-2A chain (fragment) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 478.5; DB 2; Length 135;
Best Local Similarity 74.4%; Pred. No. 1.7e-37;
Matches 90; Conservative 13; Mismatches 13; Indels 5; Gaps 1;
QY 1 QVOLKESGFLVLPSPQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDYN 60
Db 20 QVOLKQSGFLVQPSQSLSTCTVSGFSLSYGVHWVRQPPGKLEWLGVIWGGSTPDYN 79
QY 61 SALKSRLSISKDNSKNQVFLKMNSLTAADTAVVYCARKEFYGYDGFVWGQTLVTVS 120
Db 80 AAFISRLSISKDNSKQVFFKMNSLQANDTAIVYCARLTVY-----FDYWGQGTTLTVS 134
QY 121 S 121
Db 135 S 135

RESULT 10
S11100
Ig heavy chain V region (clone NQ2-20.5.3) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C/Accession: S11100
R/Kartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A/Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone
A/Reference number: S07331; MUID:83271467; PMID:6877353
A/Accession: S11100
A/Molecule type: mRNA
A/Residues: 1-112 <MAT>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>
Query Match 73.7%; Score 477; DB 2; Length 112;
Best Local Similarity 76.7%; Pred. No. 1.9e-37;
Matches 92; Conservative 8; Mismatches 12; Indels 8; Gaps 1;


```
QY      1 QVQLKESGPGLVKPSQTLSTCTTISGSHLSRYSVHWVRQPPGKGLWLGIMWGAGNTDYN 60
      2 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 QVQLKESGPGLVAPSSLSITCTVSGXSLTSGVHWVRQPPGKGLWLGILMAGSGSTNNX 60
      2 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 SALKRSLISKDNSKQVFLKMNLSLTADTAIVYCARKEGFYYGYDGFVYWGQGLTVTS 120
      62 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 SALKRSLISKDNSKQVFLKMNLSLTQDTPAMYYCAR-----DRGXVWGQGLTVTS 112
```

RESULT 11

S11101
Ig heavy chain V region (clone NQ2-48.2.2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C/Accession: S11101
R/Kaarinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A/Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazone
A/Reference number: S07331; MUID:83271467; PMID:6877353
A/Accession: S11101
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-113 <KAA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/15-97/Domain: immunoglobulin homology <IM>

Query Match

Query Match	73.7%;	Score 477;	DB 2;	Length 113;
Best Local Similarity	76.0%;	Pred. No. 1.9e-37;		
Matches 92;	Conservative	9;	Mismatches 12;	Indels 8;
				Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSITCTISGFSLSRYSVHWYRQPFGKGLEWLGMIWGSGANTDYN 60
||||| : ||||| : ||||| : ||||| : ||||| :
Db 1 QVQLKESGPGLVKPSQSLSITCTIVSGXSLTSYGVHNTFRQPPGKGLEWLGVINAGSGTNYN 60
||||| : ||||| : ||||| : ||||| : ||||| :

QY	61	SALKRSLSTKDN	SKNQVFLK	NSLTADTAVY	YCARKEGFYYGYDGFVYWGQGLTV	VS	120
			:		:		
Dh	61	SALMSRLSTKDN	SKSXVFLK	NSLOTDDTAM	YCAR-----DRGVYWGQGLTV	VS	112

QY	121	S	121
		:	
Db	113	A	113

RESULT 12

Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26470
 R:Kavaler, J.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S26459
 A:Accession: S26470
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-115 <KAV>
 A:Cross-references: EMBL:X59109; NID:g51948; PIDN:CAA41835.1; PID:g51949
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match

Query Match	73.6%;	Score 476.5;	DB 2;	Length 115;
Best Local Similarity	76.9%;	Pred. No. 2.2e-37;		
Matches 90;	Conservative 10;	Mismatches 14;	Indels 3;	Gaps 2;

```
QY      1 QVQLKESGPGLVKPSQTLSITCTTSGFSLRSYSVHWVRQPPGKLEWLGIMWGGSNTDYN 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 QVQLKQSGPGLVQPSQSLSTICTYSGFSLTSYGVHWVRQSPGKLEWLGIMWGGSNTDYN 60
```

```

QY      61 SALKSRISISKDNSKNQVFLKXNSLTAADTAIVYYCARKGEFFYYGYDG-FVYWGQGL 116
      : - - - - - : - - - - - : - - - - - : - - - - - : - - - - -
Db      61 AAFISRLSISKDNSKSQVFFKXNSLQADDTAIVYYCARKN--YYGSSXMFAYWQGQGL 115

```

RESULT 13
S11102
- mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C;Accession: S11102
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11102
A;Molecule type: mRNA
A;Residues: 1-116 <NAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match

Query Match :	73.0%;	Score 472;	DB 2;	length 116;
Best Local Similarity	75.2%;	Pred. No. 5.8e-37;		
Matches 91; Conservative	9;	Mismatches 13;	Indels 8;	Gaps 1;

OY

1 QVQLKESGPGLVKPSQGLTISCTTSIGFSLRSYSVHWVRQP PGKGLEWLGMTGGGTNDYN 60
||||| : ||||| : ||||| : ||||| : |||||
Dd

1 QVQLKESGPGLVKPSQSITCTVSXGSILSYGVHWRQPP GKGLEWLGIWAAGSTNYN 60
||||| : ||||| : ||||| : ||||| : |||||

```
QY      61 SALKERLISKDNSKNQVFLKONSLTAADTAVYYCARKEFFYYGYDGFVYWGGGLVTVS 120
        ||| ||||| : ||||| ||| ||||| |||
Db      61 SALMSRLISKDNSKSXVFLKONSLQTDPTAMYYCAR-----DRGXWGGGLVTVS 112
```

QY	121 S 121
	:
Db	113 A 113

RESULT 14

ig gamma-1 chain precursor (15C5) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S14238
R/Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A/Title: Construction and characterization of a recombinant murine monoclonal antibody di
A/Reference number: S14236; MUID:91006173; PMID:2209622
A/Accession: S14238
A/Molecule type: mRNA
A/Residues: 1-140 <VAN>
A/Cross-references: EMBL:X56392; NID:g51619; PIDN:CAA39803.1; PID:g747853
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F/26-108/Domain: immunoglobulin homology <IMM>

Query Match

Query Match	72.6%;	Score 470;	DB 2;	Length 140;
Best Local Similarity	73.6%;	Pred. No. 1.1e-36;		
Matches 89;	Conservative 13;	Mismatches 15;	Indels 4;	Gaps 2;

```
QY      1 QVQLKESGPGLVKPSQTLSTCTTISGFSLSKRYSVHWVROPFGKGLWLGMIWGCGNTDYN 60
        |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      12 QVQLKQSGPGLVQPSQSLSTCTCTVSGFSLTLYGVHWIRQSPGKGLWLGVIWVGSGTDYN 71
```

```
QY      61 SALKSRLLSIKDNKSNOVELKMNLSLTAAADTAIVYYCARKEGFYYGYDGFVYWGGILVTVS 1200
       :| | | | | : | | | | | : | | | | | : | | | | |
Db      72 AAFISRLSINKDNKSQVEFKMNSLQANDTAIYCARN---YWG-TSM DYWGQGISTVTVS 127
```

QY	121	S	121
Db	128	S	128

RESULT 15

544484 Ig heavy chain V region (4B1 VH) - mouse
C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C;Accession: S42484
R;Gilbert, D.; Brard, F.; Margartite, C.; Delpech, A.; Tron, F.
submitted to the EMBL Data Library, March 1994
A;Description: An idiotype D23-bearing polyspecific, murine anti-DNA monoclonal antibody
A;Reference number: S42484
A;Accession: S42484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <GIL>
A;Cross-references: EMBL:Z30962; NID:g461325; PIDN:CAA83216.1; PID:g461326
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match . 72.1%; Score 466.5; DB 2; Length 116;
Best Local Similarity 72.7%; Pred. No. 1.9e-36;
Matches 88; Conservative 13; Mismatches 15; Indels 5; Gaps 1;

QY	1	QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWYRQPPGKLEWLGIMGGNTDYN	60
		: : : : : : : : :	
Db	1	QVQLQESGPGLVAPSQSLSTCTVSGFSLTSYALSWVRQPPGKLEWLGVIWVGGINYN	60
QY	61	SALKSRSLISKDNSKNQVFLKNSLTAADTAVYYCARKEFFYYGYDGFVYWGQGLTVTS	120
		: : : : : : : : :	
Db	61	SALKSRSLISKDNSKSQIFLKLSLQTDADARYFCARD-----GYSFFDYWGQGLTVTS	115
QY	121	S 121	
Db	116	S 116	

Search completed: March 26, 2004, 05:08:56
Job time : 12.4433 secs

DB 80 STLKSRLLTTKDNKSKQVFLKMNLSLQTDLTARYCASVSIIYGRSDXYFTLDYWGQSTS 139
QY 117 VTVSS 121
DB 140 VTVSS 144

RESULT 2

HV44_MOUSE
ID HV44_MOUSE STANDARD; PRT; 115 AA.
AC P01820;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region PJ14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=81012133; PubMed=6774258;
RX Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
CC -! SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC EMBL; V00767; CAA24148.1; -
DR PIR; A02095; HVMS14.
DR PDB; 1A7N; 29-APR-98.
DR PDB; 1A7O; 29-APR-98.
DR PDB; 1A7P; 29-APR-98.
DR PDB; 1A7R; 29-APR-98.
DR PDB; 1G7H; 17-JAN-01.
DR PDB; 1G7I; 17-JAN-01.
DR PDB; 1G7J; 17-JAN-01.
DR PDB; 1G7M; 17-JAN-01.
DR PDB; 43C9; 24-JUL-02.
DR PDB; 43CA; 24-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.

KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 115 IG HEAVY CHAIN V REGION PJ14.
FT DOMAIN 20 >115 IG-LIKE.
FT NON TER 115
SQ SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;

Query Match 67.1%; Score 434; DB 1; Length 115;
Best Local Similarity 85.4%; Pred. No. 2.9e-38;
Matches 82; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLVGLWIGMGNTDYN 60
DB 20 QVQLKESGPGLVAPSQSLSTCTVSGFSLTGYNWVRQPPGKGLVGLWIGMGSDTDYN 79
QY 61 SALKSRLLSKDNKSKNQVFLKMNLSLTADTAVYYCA 96
DB 80 SALKSRLLSKDNKSKNQVFLKMNLSLTADTAVYYCA 115

RESULT 3

HV45_MOUSE
ID HV45_MOUSE STANDARD; PRT; 116 AA.
AC P01821;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MC101 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=82075900; PubMed=6273429;
RX Kataoka T., Miyata T., Miyata T., Moriaki K., Honjo T.;
RT "The nucleotide sequences of rearranged and germline immunoglobulin
VH genes of a mouse myeloma MC101 and evolution of VH genes in
mouse."
RL J. Biol. Chem. 257:277-285(1982).
CC -! SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC EMBL; J00502; AAA38515.1; -
DR PIR; A02096; GLMS10.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.

KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION MC101.
FT DOMAIN 20 >116 IG-LIKE.
FT NON TER 116
SQ SEQUENCE 116 AA; 12593 MW; 8079A6E87C552B3E CRC64;

Query Match 65.4%; Score 423; DB 1; Length 116;
Best Local Similarity 79.4%; Pred. No. 4.1e-37;
Matches 77; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLVGLWIGMGNTDYN 60
DB 20 QVQLKESGPGLVQPSQSLSTCTVSGFSLTGYNWVRQPPGKGLVGLWIGMGSDTDYN 79
QY 61 SALKSRLLSKDNKSKNQVFLKMNLSLTADTAVYYCAR 97
DB 80 AAFISRLSKDNKSKNQVFFKMNLSLQSDNTAIYYCAR 116

RESULT 4

HV02_XENLA
ID HV02_XENLA STANDARD; PRT; 135 AA.
AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG14 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLVGLWIGMGNTDYN 60
DB 20 QVQLKESGPGLVQPSQSLSTCTVSGFSLTGYNWVRQPPGKGLVGLWIGMGSDTDYN 79
QY 61 SALKSRLLSKDNKSKNQVFLKMNLSLTADTAVYYCAR 97
DB 80 AAFISRLSKDNKSKNQVFFKMNLSLQSDNTAIYYCAR 116

[illegible]

```
DR InterPro;IPR003596; IG_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PSS0835; IG_LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 112  
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON_TER 122 122  
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;  
  
Query Match 57.9%; Score 374.5; DB 1; Length 122;  
Best Local Similarity 55.7%; Pred. No. 4.8e-32;  
Matches 68; Conservative 24; Mismatches 29; Indels 1; Gaps 1;  
  
QY 1 QVQLKESGPGLVKPSQTLSITCTISGFSLSRYSVHWVRQPDPKGLEWLGMI-WGGNTDY 59  
|||:::||:::||:::||:::||:::||:::||:::||:::||:::||  
DB 1 QVELVESGGGVAVPGRSRLRLSCAASGFTFSNYAMHWVRQPPKGLEWVAVISBGBKYY 60  
::||:::||:::||:::||:::||:::||:::||:::||:::||  
QY 60 NSALKSRLLSKDNSKNQVFLKMNSLTADTAVIYCARKGEFYGYDGFIYWGGTLTV 119  
Db 61 ABSVKGRFTISRDSKSTLYLQMNSLRAEETAVIYCARDRPLYGBYRAFNWGGTLTV 120  
120 SS 121  
||  
DB 121 SS 122  
  
RESULT 6  
HV2I_HUMAN  
ID HV2I_HUMAN STANDARD; PRT; 146 AA.  
AC P06331;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-II region ARH-77 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85205332; PubMed=3922855;  
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;  
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence in 5' flanking region.";  
RL Gene 33:181-189.(1985).  
DR PIR; A02101; GIHMU2.  
DR HSSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PSS0835; IG_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 1 19 IG HEAVY CHAIN V-II REGION ARH-77.  
FT DOMAIN 20 146 V SEGMENT.  
FT DOMAIN 118 127 D SEGMENT.  
FT DOMAIN 128 146 J SEGMENT.  
FT DISULFID 42 115 BY SIMILARITY.  
FT NON_TER 146 146  
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;  
  
Query Match 57.3%; Score 370.5; DB 1; Length 146;  
Best Local Similarity 58.1%; Pred. No. 1.5e-31;  
Matches 75; Conservative 20; Mismatches 23; Indels 11; Gaps 3  
  
QY 1 QVQLKESGPGLVKPSQTLSITCTISGFLSRYSVHWVRQDPDKGLEWLGMIWGNTDYN 60  
||||:::|||||:::|||:::||:::||:::||:::||:::||:::||  
21 QVQLQQGWAGLVKPSSETLSLTCAVFSGGSFGSYMSWRQPPGRGLEWIGEINHSGSTNYK 80
```



```

OY      61 SALKSRLEISKDNSKNQVFLKMNSLTAADTAVYYCAR--KG-----EFGYGYDFGVYWG 112
       :|::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      81 TSLKSRVTISLDTSKNLFSLKLSSVTAADTAVYYCARGLLRGGMNDVDYYGMD---VMG 137

OY      113 QGTLVTVSS 121
       |||::|||
Db      138 QGTLVTVSS 146

RESULT 7
HV46_MOUSE STANDARD; PRT; 137 AA.
ID HV46_MOUSE
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
   gene segment.";
RL Mol. Immunol. 26:431-434(1989).
RN [2]
RP SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;
RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
   immunoglobulin heavy chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN [3]
RP SEQUENCE OF 1-21.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RL Fed. Proc. 38:1839-1845(1979).
RN [4]
RP SEQUENCE OF 19-136.
RX MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.O., Hood L., Bisen H.N.;
RT "Amino-acid sequence of the variable region of the heavy (alpha)
   chain of a mouse myeloma protein with anti-hapten activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN [5]
RP REVISION TO 53.
RX MEDLINE=77244979; PubMed=268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RT Unpublished results, cited by:
RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC -I- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
   PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC -----
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CC -----
CC EMBL; M27638; AAA61337.1; -.
DR EMBL; X07880; CAA30727.1; -.
DR PIR; PL0102; AVMS35.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

```

```

DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 137
FT DOMAIN 19 48
FT DOMAIN 49 54
FT DOMAIN 55 68
FT DOMAIN 69 84
FT DOMAIN 85 116
FT DOMAIN 117 126
FT DOMAIN 127 137
FT DISULFID 40 114
FT CONFLICT 15 15
FT CONFLICT 15 15
FT CONFLICT 77 78
FT CONFLICT 102 102
FT CONFLICT 123 123
FT NON_TER 137
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;
Query Match 56.4%; Score 365; DB 1; Length 137;
Best Local Similarity 57.9%; Pred.No. 5.3e-31;
Matches 70; Conservative 22; Mismatches 25; Indels 4; Gaps 2
QY 2 VOLKESGPGLVKPSQTLSITCTISGFSL-SRYSVHWVRPPGKGLEWLGMIWGNTDYN 60
Db 20 VLQESGPGLVKPSSQLSILTSVTGYSTSGYFMWIRQFPGNXLEWLGIKYDGNGYN 79
QY 61 SALKSRLLSKDNSKNQVFLKMSLTADTAVYYCARKEFFYYGDGFVYWGGTLTVTS 120
Db 80 PSLKNRVSVITRDTSNQFLKNSVTTEDTATYYCAQDNHLYFD---YWGQGTLTIVS 136
QY 121 S 121
Db 137 S 137
RESULT 8
HV3H_HUMAN STANDARD; PRT; 122 AA.
ID HV3H_HUMAN P01769;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update).
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human Igm immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02052; M3HUGA.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

```

FT NON TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;
Query Match 54.0%; Score 349.5; DB 1; Length 122;
Best Local Similarity 51.6%; Pred. No. 1.9e-29;
Matches 63; Conservative 27; Mismatches 31; Indels 1; Gaps 1;
QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGMI-WGGGNTDY 59
1 QVZLVZSGGAVZPGRSLRLSCAASGFSSTYAMHWVRQAPGKGLZMLSVISYBGBBZYY 60
DB 60 NSALKSRSLISKDNSKNQVFLKMSLTADTAIVYYCARKEGFYYGYDGFVYWGQTLVTV 119
61 AASVKGRFTISRBSKBTWYLEMNSLRRAENTAVYYCARSGIALGSVAGTDYWGZGTLVTI 120
QY 120 SS 121
DB 121 SS 122
RESULT 9
HV3J_HUMAN STANDARD; PRT; 121 AA.
ID HV3J_HUMAN
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region HIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE.
RP MEDLINE=79124695; PubMed=420800;
RX Chiu Y.-Y H., Lopez de Castro J.A., Poljak R.J.;
RA "Amino acid sequence of the VH region of human myeloma
RT cryoimmunoglobulin IgG H1L."
RL Biochemistry 18:553-560(1979).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02054; GIH0HL.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;
Query Match 53.9%; Score 349; DB 1; Length 121;
Best Local Similarity 52.5%; Pred. No. 2.1e-29;
Matches 64; Conservative 23; Mismatches 33; Indels 2; Gaps 2;
QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGMI-WGGGNTDY 59
1 QVKLVQAGGAVQPPGRSLRLSCAASGFTFSNYGMHWVRQAPGKLEWVAVIWNYSRTYY 60
DB 60 NSALKSRSLISKDNSKNQVFLKMSLTADTAIVYYCARKEGFYYGYDGFVYWGQTLVTV 119
61 GDSVKGRFTISRDNKRTLMZMNSLRTEDTAVYYCARDPDLTAF-SFDYWGQVLTIV 119
QY 120 SS 121
DB 120 SS 121

RESULT 10
HV2G_HUMAN STANDARD; PRT; 117 AA.
ID HV2G_HUMAN
AC P01825;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region NEWM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE.
RP MEDLINE=77242302; PubMed=407927;
RX Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
RA "Amino acid sequence of the VH region of a human myeloma
RT immunoglobulin (IgG New).";
RL Biochemistry 16:3412-3420(1977).
RN [2]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RP MEDLINE=78066916; PubMed=618887;
RX Saul F.A., Amzel L.M., Poljak R.J.;
RA "Preliminary refinement and structural analysis of the Fab fragment
RT from human immunoglobulin new at 2.0-A resolution.";
RL J. Biol. Chem. 253:585-597(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90404; GIH0UM.
DR PDB; 7FAB; 31-JAN-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 111 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT STRAND 1 3
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT TURN 30 31
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 57 59
FT STRAND 61 63
FT TURN 64 66
FT STRAND 67 72
FT TURN 73 76
FT STRAND 77 82
FT HELIX 87 89
FT STRAND 91 98
FT STRAND 104 107
FT STRAND 111 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
Query Match 53.5%; Score 346; DB 1; Length 117;
Best Local Similarity 56.6%; Pred. No. 4.2e-29;
Matches 69; Conservative 22; Mismatches 25; Indels 6; Gaps 2;
QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGMIWGGGNTDYN 60
1 QVQLKESGPGLVKPSQTLSTCTISGFSSTFSNDYYTWVRQPPGKGLWLGIVFYHGTSDDT 60
DB 1 QVQLKESGPGLVKPSQTLSTCTISGFSSTFSNDYYTWVRQPPGKGLWLGIVFYHGTSDDT 60

DR PIR; JT0508; HVMS1B.
DR PDB; 1KCS; 11-MAY-02.
DR PDB; 1KCV; 11-MAY-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match 52.3%; Score 338.5; DB 1; Length 116;
Best Local Similarity 64.9%; Pred. No. 2.5e-28;
Matches 63; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 2 VQLKESGPGLVKPSQTLSTCTISGFSL-SRYSVHWVROPKPKGLEWLGWGGNTDYN 60
DB 20 VQLQESGPDLVKPSQSLTCTVTGYSITSGYSWHWIRQFPGNKLEWGYIHYSGNTSYN 79
QY 61 SALKSRSLISKDNSKNOVFLKNSLTADTAIVYCAR 97
DB 80 PSLKSRISITRDTSKNOFLQLNSVTTEDTATYCAR 116

RESULT 14
HV2F_HUMAN STANDARD; PRT; 129 AA.

ID HV2F_HUMAN
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human immunoglobulin D."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HUMA.
DR HSSP; P01825; 7FAB.
DR GlycoSuiteDB; P01824;
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 113 IG-LIKE.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 52.2%; Score 338; DB 1; Length 129;
Best Local Similarity 53.5%; Pred. No. 3.2e-28;

Matches 69; Conservative 21; Mismatches 31; Indels 8; Gaps 3;
QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLR--YSVHWVROPKPKGLEWLGWGGNTD 58
DB 1 RLQLQESGPGLVKPSQTLSTCTIVSGGPIRRTGYWGWIRQPKGLEWIGVYTGSIY 60
QY 59 YNSALKSRISISKDNSKNOVFLKNSLTADTAIVYCAR-KGEFYGYG-----DGFYWG 112
DB 61 YNPSLRGRVTISVDTSRNQFSLNIRMSAADTAIVYCARNDPPYYDICTGSDGDIVWG 120
QY 113 QGTLVTWSS 121
DB 121 QGTLVHSS 129

RESULT 15
HV3K_HUMAN STANDARD; PRT; 126 AA.

ID HV3K_HUMAN
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marguaret M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A and 1.0-A resolution."
RL J. Mol. Biol. 141:369-391(1980).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02055; G1HUKL.
DR PDB; 2FB4; 12-JUL-89.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT TURN 29 31
FT HELIX 34 39
FT STRAND 41 42
FT TURN 45 51
FT STRAND 53 54
FT TURN 58 60
FT STRAND 62 64
FT HELIX 65 65
FT STRAND 66 67
FT TURN 68 73

FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON TER 126 126
SQ SEQUENCE 126 AA; 13718 MM; E4D71B52B16F8776 CRC64;

Query Match 51.9%; Score 335.5; DB 1; Length 126;
Best Local Similarity 51.9%; Pred. No. 5.7e-28;
Matches 68; Conservative 22; Mismatches 26; Indels 15; Gaps 4;

QY 1 QVQLKESGPGGLVKPSQTLSTICTISGFSLSRYSVHWVRQPPGKGLWLGMIW-GGNTDY 59
Db 1 QVQLVESGGGVVQPGRSRLRLSCSSSGFIFSSYAMWVRQAPGKGLWVAIIMDDGSDQHY 60
QY 60 NSALKRSLISKDNSKQNVFLKNSLTADTAVYYCARKEFFYYGDFV-----Y 110
Db 61 ADSVKGKRFITSRDNSKNTLFLQMDSLRPEDTGYYFCARDG----GH-GFCSSASCFGPDY 115
QY 111 WGQGTLLVTSS 121
Db 116 WGQGTPTVTSS 126

Search completed: March 26, 2004, 05:04:47
Job time : 8.29433 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:13 ; Search time 34.9699 Seconds
(without alignments)
1091.732 Million cell updates/sec

Title: US-10-056-052a-20
Perfect score: 647
Sequence: 1 QVQLKESGPGLVKPSQTLIS.....YGYDGFVYWGQITLVVSS 121

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvivirus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465.5	71.9	121	11 Q99NG4	Q99ng4 mus musculus
2	463.5	71.6	482	11 Q91X92	Q91x92 mus musculus
3	413	63.8	119	4 Q9UL73	Q9ul73 homo sapien
4	402.5	62.2	613	4 Q96EY0	Q96ey0 homo sapien
5	385.5	59.6	496	4 Q96KX8	Q96kx8 homo sapien
6	382.5	59.1	118	11 Q81IU5	Q81iu5 mus musculus
7	382.5	59.1	478	4 Q7Z379	Q7z379 homo sapien
8	382	59.0	492	4 Q7Z374	Q7z374 homo sapien
9	373.5	57.7	150	4 Q95973	Q95973 homo sapien
10	369	57.0	479	11 Q99M22	Q99m22 mus musculus
11	368	56.9	139	4 Q86SX2	Q86sx2 homo sapien
12	363.5	56.2	573	4 Q8WU38	Q8wu38 homo sapien
13	363	56.1	121	4 Q9UL96	Q9ul96 homo sapien
14	359	55.5	121	4 Q9UL71	Q9ul71 homo sapien
15	355.5	54.9	613	4 Q8WUK1	Q8wuk1 homo sapien
16	355	54.9	493	4 Q8NCL6	Q8ncl6 homo sapien

17	354	54.7	588	4 Q8WUX4	Q8wux4 homo sapien
18	354	54.7	597	4 Q9BU10	Q9bu10 homo sapien
19	354	54.7	618	4 Q96AA6	Q96aa6 homo sapien
20	352.5	54.5	130	4 Q8IZD7	Q8izd7 homo sapien
21	351	54.3	116	4 Q9UL93	Q9ul93 homo sapien
22	350.5	54.2	122	4 Q9UL75	Q9ul75 homo sapien
23	350.5	54.2	147	4 Q9Y509	Q9y509 homo sapien
24	350	54.1	597	4 Q9BQB8	Q9bqb8 homo sapien
25	350	54.1	597	4 Q96BB9	Q96bb9 homo sapien
26	346.5	53.6	469	11 Q8R3V9	Q8r3v9 mus musculus
27	345.5	53.4	473	4 Q8TC63	Q8tc63 homo sapien
28	344	53.2	113	4 Q9UL90	Q9ul90 homo sapien
29	343.5	53.1	112	4 Q9HCC1	Q9hcc1 homo sapien
30	337.5	52.2	118	4 Q9UL72	Q9ul72 homo sapien
31	337	52.1	119	11 Q920E7	Q920e7 mus musculus
32	336	51.9	473	11 Q9D8L4	Q9d8l4 mus musculus
33	334.5	51.7	116	4 Q7Z3Y6	Q7z3y6 homo sapien
34	333	51.5	131	4 Q9UL88	Q9ul88 homo sapien
35	332.5	51.4	122	4 Q9UL84	Q9ul84 homo sapien
36	331.5	51.2	487	11 Q99XA4	Q99xa4 mus sapien
37	330.5	51.1	494	4 Q96K68	Q96k68 homo sapien
38	324.5	50.2	298	11 Q9QYF0	Q9qyf0 mus musculus
39	322	49.8	470	4 Q7Z5W1	Q7z5w1 homo sapien
40	321	49.6	499	4 Q8N5K4	Q8n5k4 homo sapien
41	319.5	49.4	118	4 Q9UL91	Q9ul91 homo sapien
42	319.5	49.4	136	11 Q7TPE3	Q7tpe3 mus musculus
43	318.5	49.2	484	11 Q8VEA0	Q8vea0 mus musculus
44	317.5	49.1	124	6 Q9N0W6	Q9n0w6 oryctolagus
45	316.5	48.9	124	6 Q9N0W4	Q9n0w4 oryctolagus

ALIGNMENTS

RESULT 1

Q99NG4 PRELIMINARY; PRT; 121 AA.
ID Q99NG4
AC Q99NG4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
OG Plasmid PHEN1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
Bautsch W., Kola A., Kios A., Koehl J.,
RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries."
RL J. Immunol. 160:2947-2958(1998).
DR EMBL; AJ222590; CAA10890.1; ..
DR PIR; F33932; F33932.
DR HSSP; P01825; 7FAB.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Plasmid.
KW NON_TER
FT NON_TER
SQ SEQUENCE 121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;
Query Match 71.9%; Score 465.5; DB 11; Length 121;
Best Local Similarity 74.0%; Pred. No. 6.5e-43;
Matches 91; Conservative 9; Mismatches 18; Indels 5; Gaps 2;

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QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGSNTDYN 60
Db 1 QVQLKESGPGLVAPSQSLSTCTVSGFPLTSHGVSWMRQPPGKGLEWLGVIWGDGNTKYH 60
QY 61 SALKSRSLISKDNKSNQVFLKNSLTAAADTAVYYCARKGEFYGYDGFV--YWGQGLVT 118
Db 61 SALKSRSLISKDNKSNQVFLKNSLTAAADTAVYYCARKGEFYGYDGFV--YWGQGLVT 117
QY 119 VSS 121
Db 118 VSS 120

RESULT 2
Q91X92 PRELIMINARY; PRT; 482 AA.
AC Q91X92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC01181; AAH1181.1; -.
DR PIR; F33932; F33932.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;

Query Match
Best Local Similarity 71.6%; Score 463.5; DB 11; Length 482;
Matches 91; Conservative 11; Mismatches 15; Indels 5; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGSNTDYN 60
Db 20 QVQLKESGPDLVAPSQSLSTCTVSGFALTYSIAISWVRQPPGKGLEWLGVIWGTGNTYNN 79
QY 61 SALKSRSLISKDNKSNQVFLKNSLTAAADTAVYYCARKGEFYGYDGFV-YWGQGLVT 119
Db 80 SALKSRSLISKDNKSNQVFLKNSLTAAADTAVYYCARKGEFYGYDGFV-YWGQGLVT 135
QY 120 SS 121
Db 136 SS 137

RESULT 3
Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035041; AAD56277.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Query Match
Best Local Similarity 63.8%; Score 413; DB 4; Length 119;
Matches 81; Conservative 16; Mismatches 20; Indels 6; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGSNTDYN 60
Db 1 QVQLKESGPGLVKPSQTLSTCTVSGGSIYSYWSWIRQPPGKGLEWIGIYYSGSTNYT 60
QY 61 SALKSRSLISKDNKSNQVFLKNSLTAAADTAVYYCARKGEF--YGYDGFVYWGQGLVT 118
Db 61 SALKSRVTLISVDRSKNQFSLKLTSLTAAADTAVYFCARLSNWGPY---FDYWGQGLVT 116
QY 119 VSS 121
Db 117 VSS 119

RESULT 4
Q96EY0 PRELIMINARY; PRT; 613 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell1;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.1; -.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match
Best Local Similarity 62.2%; Score 402.5; DB 4; Length 613;
Matches 78; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGSNTDYN 60
Db 20 QVQLKESGPGLVKPSQTLSTCTVSGGSIYSYWSWIRQPPGKGLEWIGRIYTSGSTNYN 79
QY 61 SALKSRSLISKDNKSNQVFLKNSLTAAADTAVYYCARKGEFYGYDGFVYWGQGLVTYS 120
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Db 80 PSLKSRVTMSVDTSKNQPSLKLSSVTATADTAVYYCASQ-PNELPTVGLFYWGQGLTVVS 138
QY 121 S 121
Db 139 S 139

RESULT 5

Q96KX8 PRELIMINARY; PRT; 496 AA.
AC Q96KX8; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 59.6%; Score 385.5; DB 4; Length 496;
Best Local Similarity 62.9%; Pred. No. 2.1e-33;
Matches 78; Conservative 18; Mismatches 25; Indels 3; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLISITCTISGFSLSRVSVH--WVRQPPGKGLWLGMIWGGNTD 58
Db 20 QIQIQESGPGLVKSSFTLSITCTVSGSSISSSYWGWIROPKGLMIANTYYSGITY 79
QY 59 YNSALKSRLSISKDNSKNQVFLKMSLTAAADTAVYYCARKEFFYYGDFV-YWGQGLTV 117
Db 80 YNPSLKSRLVTISVDTSKNQPSLKLSSVTATADTAVYFCARHGYSRSGRTGAIIDYWGQGLTV 139
QY 118 TVSS 121
Db 140 TVSS 143

RESULT 6

Q81IUS PRELIMINARY; PRT; 118 AA.
AC Q81IUS; 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Anti-human Fc gamma receptor III 3G8 gamma heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Bruenke J., Valerius T., Repp R., Fey G.H.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY173025; AA018227.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12979 MW; F57BB07033742E99 CRC64;

Query Match 59.1%; Score 382.5; DB 11; Length 118;
Best Local Similarity 62.6%; Pred. No. 7.2e-34;
Matches 77; Conservative 13; Mismatches 26; Indels 7; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLISITCTISGFSL--SRYSVHWVRQPPGKGLWLGMIWGGNTD 58
Db 1 QVTLKESGPGILQPSQTLISLTCSFGFSLFTSGMGVGIROPKGLMIWDDDKR 60
QY 59 YNSALKSRLSISKDNSKNQVFLKMSLTAAADTAVYYCARKEFFYYGDFVYWGQGLTV 118
Db 61 YNPALKSRLTISKDTSSNQVFLKIASVDTADTAVYCAQINPAW----PAYWGQGLTV 115
QY 119 VSS 121
Db 116 VSA 118

RESULT 7

Q7Z379 PRELIMINARY; PRT; 478 AA.
AC Q7Z379; 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN DKFZP686K04218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 59.1%; Score 382.5; DB 4; Length 478;
Best Local Similarity 63.4%; Pred. No. 4.2e-33;
Matches 78; Conservative 16; Mismatches 24; Indels 5; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLISITCTISGFSLSR--YSVHWVRQPPGKGLWLGMIWGGNTD 58
Db 19 QVQLQESGPGLVKPSQTLISLTCTVSGSIGSGDYFWSGIROPKGLWGMGYIYSGSTY 78
QY 59 YNSALKSRLSISKDNSKNQVFLKMSLTAAADTAVYYCARKEFFYYGDFVYWGQGLTV 118
Db 79 YNPSLKSRLSISIDTSKNQFSRLNSLTAAADTAVYFCARGVGLGTAFD---IMGQGLVTV 135
QY 119 VSS 121
Db 136 VSS 138

RESULT 8

Q7Z374 PRELIMINARY; PRT; 492 AA.
ID Q7Z374


```
AC 072374;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN DKFZP686C02218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Robo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match
Best Local Similarity 59.0%; Score 382; DB 4; Length 492;
Matches 78; Conservative 16; Mismatches 25; Indels 4; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSL--RYSVHWVRQPPGKLEWLGMIWGNTD 58
DB 32 QLOQESGPGLVKPSSETLSLCTVSGSVSNRNYWGMIRQPPGKLEWIGSIYVENTY 91

QY 59 YNSALKSRSLISKDINSKQVFLKMSLTADTAIVYYCARKEFFYYGDFVYWGQGLVT 118
DB 92 YSPSLKSRLLTFVDTSKNHFLRLTSVTAADTAIVYYCVRHVEGPGYGM--FDPWGQGLVT 149

QY 119 VSS 121
DB 150 VSS 152

RESULT 9
ID 095973 PRELIMINARY; PRT; 150 AA.
AC 095973;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of IGM secreting B cell in the synovium of
RT Behcet's patient with arthritis.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1
FT CHAIN 20 >150 POTENTIAL.
FT NON_TER 150 VH4 HEAVY CHAIN VARIABLE REGION.
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match
Best Local Similarity 57.7%; Score 373.5; DB 4; Length 150;
Matches 73; Conservative 20; Mismatches 23; Indels 7; Gaps 2;
```

```
QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSL--RYSVHWVRQPPGKLEWLGMIWGNTD 58
DB 20 QLOQESGPGLVKPSSETLSLCTVSGSVSNRNYWGMIRQPPGKLEWIGSLHNSGSDY 79

QY 59 YNSALKSRSLISKDINSKQVFLKMSLTADTAIVYYCARKEFFYYGDFVYWGQGLVT 118
DB 80 YNSPSLSRVTISVDTSKNQPSRLSSVTAADTAIVYYCAR-----LGMGAFDFGHGTMVT 134

QY 119 VSS 121
DB 135 VSS 137

RESULT 10
ID 099M22 PRELIMINARY; PRT; 479 AA.
AC 099M22;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002091; AAH02091.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match
Best Local Similarity 57.0%; Score 369; DB 11; Length 479;
Matches 71; Conservative 22; Mismatches 22; Indels 6; Gaps 2;

QY 2 VQLKESGPGLVKPSQTLSTCTISGFSL--SRYSVHWVRQPPGKLEWLGMIWGNTDYN 60
DB 20 VQLQESGPGLVKPSQSLSLCTSVTGYSITSGYWNWIRQPPGKLEWIGYINYSNNYN 79

QY 61 SALKSRSLISKDINSKQVFLKMSLTADTAIVYYCARKEFFYYGDFVYWGQGLTVS 120
DB 80 PSUKNRISITRDTSKNQVFLKINSVTTEDTATYYCASR-----GYSWFPNWGQGLTVS 134

QY 121 S 121
DB 135 A 135

RESULT 11
ID 086SX2 PRELIMINARY; PRT; 139 AA.
AC 086SX2;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Human full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line)
DE of Homo sapiens (Human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Genoscope; (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RT "Full-length cDNA libraries and normalization.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Plasmid.
KM NON TER
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 56.9%; Score 368; DB 4; Length 139;
Best Local Similarity 70.1%; Pred. No. 3.4e-32;
Matches 68; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLVWLIMGGNTDYN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 33 QVQLQESGPGLVKPSSETSLTCTVSGGSISSYSWMTIQPPGKGLIEWIGIYSGSTNYN 92

QY 61 SALKSRSLISKDNSKNQVFLKMSLTADTAIVYYCAR 97
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 93 PSLSKRVTTISVDTSKNQFSLKLSVTADTAIVYYCAR 129

RESULT 12
Q8WU38 PRELIMINARY; PRT; 573 AA.
ID Q8WU38; AC Q8WU38;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -.
DR PIR; S21205; S21205.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 56.2%; Score 363.5; DB 4; Length 573;
Best Local Similarity 53.5%; Pred. No. 6.3e-31;
Matches 68; Conservative 23; Mismatches 27; Indels 9; Gaps 3;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLVWLIMGGNTDYN 59
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLVESGGGLVQPGSRSLRLSCAASGFTPDYAMHWVRQAPGKGLVWVSGISWNSGSIgy 79

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QY      NSALKSRLSISKDNSKNQVFLKMSLTADTAVYYCARKE-----FYGVDGFVWGGG 114
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      ADSVKGRFTISRDNAKNSLYLQMNSLRADTLALYYCAKHGSGSYIGYYGMD---VMGQG 136

QY      115 TLVTVSS 121
          |||||
Db      137 TTVTVSS 143

RESULT 13
Q9UL96      PRELIMINARY; PRT; 121 AA.
ID Q9UL96;
AC Q9UL96;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RI Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035018; AAD56254.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match      56.1%; Score 363; DB 4; Length 121;
Best Local Similarity 60.0%; Pred. No. 1e-31;
Matches 75; Conservative 15; Mismatches 27; Indels 8; Gaps 3;

QY      1 QVQLKESGPGLVKPSQSLTSITCTISGFSL--SRYSVHWVQPEGKGLEWLGIMWGNTD 58
          |:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      1 QITLKESGPVLVKPTQTLLTCTPSGFSLTSGMDVGWIRQDPGKALEWLALITYWDPPKR 60

QY      59 YNSALKSRLSISKDNSKNQVFLKMSLTAA DTAVYYCA--RKGEFYGYDGFFVWGGGT 116
          |:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 YSPSLKSRLTITTKDTSKNQVDLTMTFMDPWTATYYCAHRSKSDGYX----FDYWGGGT 116

QY      117 VTVSS 121
          |||||
Db      117 VTVSS 121

RESULT 14
Q9UL71      PRELIMINARY; PRT; 121 AA.
ID Q9UL71;
AC Q9UL71;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```

RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA "Yosin-D.C.,
 RT "Mysin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035043; AAD56279.1; -.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 121
 SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match	55.5%	Score 359;	DB 4;	Length 121;
Best Local Similarity	57.4%	Pred. No. 2.7e-31;		
Matches 70;	Conservative 21;	Mismatches 29;	Indels 2;	Gaps 2;

[illegible]

QY	120	SS	121
Db	120	SS	121

RESULT 15

ID	Q8WUK1	PRELIMINARY;	PRT;	613 AA.
AC	Q8WUK1;			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Tonsil;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC020240; AA020240.1; -.			
DR	PIR; P0120; P0120.			
DR	PIR; S15590; S15590.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IG; 5.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 5.			
DR	PROSITE; PS00290; IG_MHC; 3.			
KW	Hypothetical protein.			
SQ	SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;			

Query Match	54.9%	Score 355.5;	DB 4;	Length 613;
Best Local Similarity	55.7%	Pred. No. 5.1e-30;		
Matches 68;	Conservative 23;	Mismatches 28;	Indels 3;	Gaps 2;

```
QY      1 QVQLKESGPGLVKPSQTLSTICTTISGFSLSRYSVHWVRQPPGKGLEWLGMI-WGGGNTDY 59
      |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db      20 QVQLVESGGGVQPGKSLRLSCAASGFTFSISYGMHWVRQAPGKGLEWVAIVISYDSNKKY 79
QY      60 NSALKSRSLISKDNSKNQVFLKMNSLTAADTAVVYCARKEGFYIGYDGFVTVWGQGLITV 119
```

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Db      80  ADSVKGREFTISRDN SKNTLYLQMSLRADETAVVYCAK--DWSEGVETFDIMGQGTMTV 137
QY      120  SS 121
        ||
Db      138  SS 139

```

```
Search completed: March 26, 2004, 05:07:48
Job time : 36.9699 secs
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:51:26 ; Search time 6.75177 Seconds
(without alignments)
863.752 Million cell updates/sec

Title: US-10-056-052a-18
Perfect score: 583
Sequence: 1 DIVMTQSPDSLAVSLGERVT.....YCHQYLSSYTFGGTKLEIK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521	89.4	133	1	KV4B_HUMAN P06313 homo sapien
2	520.5	89.3	114	1	KV4A_HUMAN P01625 homo sapien
3	505.5	86.7	134	1	KV4C_HUMAN P06314 homo sapien
4	479	82.2	121	1	KV40_HUMAN P06312 homo sapien
5	467.5	80.2	109	1	KV4D_HUMAN P83593 homo sapien
6	388.5	66.6	136	1	KV5B_MOUSE P01634 mus musculu
7	387	66.4	110	1	KV3P_MOUSE P01668 mus musculu
8	384.5	66.0	111	1	KV3L_MOUSE P01664 mus musculu
9	381	65.4	129	1	KV3L_HUMAN P18135 homo sapien
10	381	65.4	129	1	KV3M_HUMAN P18136 homo sapien
11	379.5	65.1	149	1	KV5A_MOUSE P01633 mus musculu
12	377	64.7	109	1	KV3B_HUMAN P01622 homo sapien
13	376	64.5	109	1	KV3D_HUMAN P01620 homo sapien
14	375.5	64.4	114	1	KV1A_MOUSE P01605 homo sapien
15	374.5	64.2	108	1	KV1M_HUMAN P01603 mus musculu
16	374	64.2	109	1	KV3E_HUMAN P01623 homo sapien
17	373.5	64.1	111	1	KV3O_MOUSE P01665 mus musculu
18	373.5	64.1	111	1	KV3O_MOUSE P01665 mus musculu
19	372.5	63.9	111	1	KV3H_MOUSE P01660 mus musculu
20	372	63.8	129	1	KV3H_HUMAN P04207 homo sapien
21	367.5	63.0	111	1	KV3R_MOUSE P01666 mus musculu
22	367.5	63.0	111	1	KV3R_MOUSE P01670 mus musculu
23	367.5	63.0	129	1	KV1W_HUMAN P04431 homo sapien
24	367	63.0	108	1	KV3A_HUMAN P01619 homo sapien
25	367	63.0	109	1	KV3F_HUMAN P01624 homo sapien
26	366.5	62.9	111	1	KV3J_MOUSE P01662 mus musculu
27	366	62.8	133	1	KV2F_HUMAN P06310 homo sapien
28	365.5	62.7	111	1	KV3Q_MOUSE P01669 mus musculu
29	365.5	62.7	111	1	KV3U_MOUSE P01673 mus musculu
30	365	62.6	113	1	KV2B_HUMAN P01615 homo sapien
31	365	62.6	113	1	KV2G_MOUSE P01631 mus musculu
32	364.5	62.5	108	1	KV1V_HUMAN P04430 homo sapien
33	364.5	62.5	108	1	KV1Y_HUMAN P80362 homo sapien

34	364.5	62.5	115	1	KV2A_HUMAN P01614 homo sapien
35	364	62.4	117	1	KV2E_HUMAN P06309 homo sapien
36	362.5	62.2	108	1	KV1H_HUMAN P01600 homo sapien
37	362	62.1	107	1	KV1D_HUMAN P01596 homo sapien
38	362	62.1	109	1	KV3G_HUMAN P04206 homo sapien
39	361.5	62.0	131	1	KV3I_MOUSE P01661 mus musculu
40	360.5	61.8	108	1	KV1K_HUMAN P01603 homo sapien
41	360.5	61.8	108	1	KV1O_HUMAN P01607 homo sapien
42	360.5	61.8	111	1	KV3S_MOUSE P01671 mus musculu
43	360.5	61.8	128	1	KV3K_HUMAN P06311 homo sapien
44	359	61.6	113	1	KV2D_HUMAN P01617 homo sapien
45	358.5	61.5	111	1	KV3T_MOUSE P01672 mus musculu

ALIGNMENTS

RESULT 1					
ID	KV4B_HUMAN	STANDARD;	PRT;	133	AA.
AC	P06313				
DT	01-JAN-1988 (Rel. 06, Created)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-IV region JI precursor.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86041853; PubMed=2997712;				
RA	Klobeck H.G., Bornkamm G.W., Combriato G., Moclkat R., Pohlenz H.D.,				
RA	Zachau H.G.;				
RT	"Subgroup IV of human immunoglobulin K light chains is encoded by a				
RL	single germline gene."				
RL	Nucleic Acids Res. 13:6515-6523(1985).				
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CC	EMBL; Z00022; CAA77317.1; .				
DR	PIR; A01904; KAHUUI.				
DR	HSSP; P80362; 1WTL.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; F:antigen binding; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; IG-like.				
DR	InterPro; IPR003596; IG_v.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Immunoglobulin V.region; Signal.				
FT	SIGNAL	1	20		
FT	CHAIN	21	133		IG KAPPA CHAIN V-IV REGION JI.
FT	DOMAIN	21	43		FRAMEWORK-1.
FT	DOMAIN	44	60		COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	61	75		FRAMEWORK-2.
FT	DOMAIN	76	82		COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	83	114		FRAMEWORK-3.
FT	DOMAIN	115	122		COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	123	132		FRAMEWORK-4.
FT	DISULFID	43	114		BY SIMILARITY.
FT	NON TER	133	133		
SQ	SEQUENCE	133	AA;	14632	MM; SFB3953066744AF4 CRC64;
Query Match 89.4%; Score 521; DB 1; Length 133;					
Best Local Similarity 89.3%; Pred. No. 1.5e-48;					

Matches 100; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERVTMNCSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
DB 21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQOKPGQPPKLLIYMASTR 80
QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSYTFGGGTGLEIK 112
DB 81 ESGVPDRFSGSGSGTDFTLTITSSLSQAEDVAVYYCCQYDTIPTFGGKTVEIK 132

RESULT 2

KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;

Submitted (AUG-1996) to Swiss-Prot.

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PDB; 1EEQ; 01-FEB-01.
DR PDB; 1EEU; 03-FEB-01.
DR PDB; 1EFQ; 09-FEB-01.
DR PDB; 1EK3; 06-MAR-01.
DR PDB; 1LVE; 21-JAN-98.
DR PDB; 3LVE; 18-MAY-99.
DR PDB; 5LVE; 28-MAR-01.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.

FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 113 FRAMEWORK-4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 89.3%; Score 520.5; DB 1; Length 114;

Best Local Similarity 89.4%; Pred. No. 1.4e-48;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMNCSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
DB 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQOKPGQPPKLLIYMASTR 60

QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSYTFGGGTGLEIK 112
DB 81 ESGVPDRFSGSGSGTDFTLTITSSLSQAEDVAVYYCCQYDTIPTFGGKTVEIK 132

DB 61 ESGVPDRFSGSGSGTDFTLTITSSLSQAEDVAVYYCCQYSTPYPFGGKTVEIK 113

RESULT 3

KV4C_HUMAN STANDARD; PRT; 134 AA.
ID P06314;
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1998 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;

Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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CC EMBL; X02990; CAA26733.1; -.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 86.7%; Score 505.5; DB 1; Length 134;

Best Local Similarity 85.8%; Pred. No. 6.7e-47;
Matches 97; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMNCSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
DB 21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSDNKNYLAWYQOKPGQPPKLLIYMASTR 80

QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSYTFGGGTGLEIK 112
DB 81 ESGVPDRFSGSGSGTDFTLTITSSLSQAEDVAVYYCCQYNNLPWTFGGGTVEIK 133

RESULT 4

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KV40_HUMAN
ID_KV40_HUMAN STANDARD; PRT; 121 AA.
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN IGKV4-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -1- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
CC -----
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CC -----
CC EMBL; Z00023; CAA77318.1; -.
DR DR PIR; A01902; K4HU.
DR DR HSSP; P80362; 1WTL.
DR DR Genew; HGNC:5834; IGKV4-1.
DR DR GO; GO:0005576; C:extracellular; NAS.
DR DR GO; GO:0003823; P:antigen binding; NAS.
DR DR GO; GO:0006955; P:immune response; NAS.
DR DR InterPro; IPR007110; Ig-like.
DR DR InterPro; IPR003596; Ig_v.
DR DR Pfam; PF00047; Ig; 1.
DR DR SMART; SM00406; IGV; 1.
DR DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 >121 IG KAPPA CHAIN V-IV REGION.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD418D33974 CRC64;

Query Match 82.2%; Score 479; DB 1; Length 121;
Best Local Similarity 91.0%; Pred. No. 4e-44;
Matches 91; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERVTMNCSSQSVLYSSNKNYLAHYQOKPGQSPKLLIYMASTR 60
DB 21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNKNYLAHYQOKPGQPKLLIYMASTR 80
QY 61 ESGVPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLS 100
DB 81 ESGVPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLS 120

RESULT 5
KV4D_HUMAN STANDARD; PRT; 109 AA.
ID_KV4D_HUMAN
AC P83593;
DT 10-OCT-2003 (Rel. 42, Created)
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DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-IV region STH (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Abdominal adipose tissue;
RX MEDLINE=98249779; PubMed=9588180;
RA Olsen K.E., Sletten K., Westermarck P.;
RT "Extended analysis of Al-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -1- FUNCTION: May play an important role in fibrillogenesis.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00409; IG; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 101 FRAMEWORK-4.
FT DOMAIN 102 109 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 94 BY SIMILARITY.
FT UNSURE 23 23
FT UNSURE 94 94
FT NON TER 109 109
SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;

Query Match 80.2%; Score 467.5; DB 1; Length 109;
Best Local Similarity 82.6%; Pred. No. 5.9e-43;
Matches 90; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMNCSSQSVLYSSNKNYLAHYQOKPGQSPKLLIYMASTR 60
DB 1 DIVMTQSPDSLAVSLGERATINCRSSQSVLYSSNKNYLAHYQOKPGQAPKLLIFSWASTR 60
QY 61 ESGVPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLS-SYTFGGGTK 108
DB 61 ESGVPDRFSGSGGTDFLTITPGLQAEDLAVYYCHQYRIPYTFGGGAK 109

RESULT 6
KV5B_MOUSE STANDARD; PRT; 136 AA.
ID_KV5B_MOUSE
AC P01634;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-V region MOPC 21 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Galt M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [2]
RP SEQUENCE OF 30-136.
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
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[illegible][illegible]


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RT genes.";
RL Can. J. Biochem. 58:176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RL myeloma MPC 11.";
CC Biochem. J. 171:337-347(1978).
CC -I- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
CC -----
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CC -----
DR EMBL; J00561; AAA38776.1; -.
DR PIR; A90823; KVM311.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MPC11.
FT DOMAIN 42 64 FRAMEWORK-1.
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 76 90 FRAMEWORK-2.
FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 129 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 130 138 FRAMEWORK-3.
FT DOMAIN 139 148 COMPLEMENTARITY-DETERMINING-4.
FT REPEAT 26 35
FT REPEAT 38 47
FT NON TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match
Best Local Similarity 65.1%; Score 379.5; DB 1; Length 149;
Matches 78; Conservative 12; Mismatches 16; Indels 7; Gaps 2;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNQNYLAHYQOKPGQSPKLLIYNASTR 60
DB 42 DIVMTQSHKFMSTSVGDRVSITCKASQDV-----STTVAMYQOKPGQSPKLLIYSASYSR 95
QY 61 ESGVPPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLLS-YTFGGGTKLEIK 112
DB 96 YTGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCCQHYSTPPTFGGGTKLEIK 148

RESULT 12
KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
```

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RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IGM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC -----
DR PIR; A01892; K3HUS1.
DR HSSP; P80362; 1MTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match
Best Local Similarity 64.7%; Score 377; DB 1; Length 109;
Matches 73; Conservative 20; Mismatches 14; Indels 6; Gaps 2;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNQNYLAHYQOKPGQSPKLLIYNASTR 60
DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSV-----SNSYLAHYQOKPGQAPRLITYGASSR 55
QY 61 ESGVPPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLLS-YTFGGGTKLEIK 112
DB 56 ATGIPDRFSGSGSGTDFTLTITSLRLPDDFAVYYCCQYGGSSPQTFGGSKVEIK 108

RESULT 13
KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region T1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT T1). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production.";
RL Hoppe-Seyler's Z. physiol. Chem. 353:189-208(1972).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -----
DR PIR; A01895; K3HUT1.
DR HSSP; P80362; 1MTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDCT7749BC CRC64;
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:58:13 ; Search time 32.3688 Seconds
(without alignments)
1091.732 Million cell updates/sec

Title: US-10-056-052a-18
Perfect score: 583
Sequence: 1 DIVMTQSPDSLAVSLGERVT.....YCHQYLSSYTFGGGTKLEIK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvrius:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	432.5	74.2	107	11 Q9ERZ9	Q9erz9 mus musculu
2	391	67.1	109	4 Q9UL78	Q9ul78 homo sapien
3	389	66.7	107	4 Q96SA9	Q96sa9 homo sapien
4	383	65.7	238	11 Q99M37	Q99m37 mus musculu
5	378.5	64.9	108	4 Q9UL70	Q9ul70 homo sapien
6	378	64.8	109	4 Q9UL85	Q9ul85 homo sapien
7	377	64.7	238	11 Q8VCI6	Q8vcic6 mus musculu
8	376.5	64.6	108	4 Q9UL77	Q9ul77 homo sapien
9	376.5	64.6	111	11 Q920E9	Q920e9 mus musculu
10	376	64.5	107	4 Q9UL81	Q9ul81 homo sapien
11	372.5	63.9	108	4 Q9UL83	Q9ul83 homo sapien
12	371.5	63.7	108	4 Q9UL79	Q9ul79 homo sapien
13	369	63.3	239	4 Q8NEK0	Q8nek0 homo sapien
14	367	63.0	109	4 Q9UL86	Q9ul86 homo sapien
15	366	62.8	239	11 Q8VC55	Q8vc55 mus musculu
16	363.5	62.3	99	11 Q9UL74	Q9j174 mus musculu

17	363.5	62.3	108	11 Q8VJ10	Q8vj10 mus musculu
18	362	62.1	243	11 Q7TQM2	Q7tqm2 mus musculu
19	360.5	61.8	236	4 Q7Z3Y4	Q7z3y4 homo sapien
20	359	61.6	239	11 Q8K0F8	Q8k0f8 mus musculu
21	358.5	61.5	111	11 Q81U6	Q81u6 mus musculu
22	355.5	61.0	234	4 Q7Z473	Q7z473 homo sapien
23	355.5	61.0	236	11 Q7TMK3	Q7tmk3 mus musculu
24	353.5	60.6	114	4 Q9UL80	Q9ul80 homo sapien
25	350	60.0	239	4 Q8TCD0	Q8tc00 homo sapien
26	349	59.9	104	11 Q9JL82	Q9j182 mus musculu
27	345.5	59.3	236	11 Q7TS98	Q7ts98 mus musculu
28	344.5	59.1	233	11 Q91WS9	Q91ws9 mus musculu
29	343	58.8	112	11 Q8K1F3	Q8k1f3 mus musculu
30	342.5	58.7	131	11 Q81IC3	Q81ic3 mus musculu
31	341.5	58.6	214	11 Q8R1A5	Q8r1a5 mus musculu
32	341	58.5	114	11 Q8K1F1	Q8k1f1 mus musculu
33	336.5	57.7	237	13 Q7SZ36	Q7sz36 xenopus lae
34	335.5	57.5	234	11 Q8R062	Q8r062 mus musculu
35	335.5	57.5	298	11 Q9QYF0	Q9qyf0 mus musculu
36	333.5	57.2	109	11 Q920E6	Q920e6 mus musculu
37	333	57.1	134	11 Q8VDD0	Q8vdd0 mus musculu
38	333	57.1	235	11 Q7TMK0	Q7tmk0 mus musculu
39	321.5	55.1	103	11 Q9JL80	Q9j180 mus musculu
40	320.5	55.0	107	11 Q9JL84	Q9j184 mus musculu
41	320.5	55.0	116	4 Q96PF6	Q96pf6 homo sapien
42	320.5	55.0	234	11 Q91WF8	Q91wf8 mus musculu
43	319	54.7	112	11 Q8K1F2	Q8k1f2 mus musculu
44	315.5	54.1	101	11 Q9JL78	Q9j178 mus musculu
45	313	53.7	106	5 Q9U410	Q9u410 schistosoma

ALIGNMENTS

RESULT 1

Q9ERZ9 PRELIMINARY; PRT; 107 AA.
ID Q9ERZ9
AC Q9ERZ9;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Anti human TNF-alpha light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
genes of an anti-hTNF-a monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
human TNF-alpha specific monoclonal antibody.";
RL Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF262753; AAG23804.1; -.
DR PDB; 2AP2; 24-NOV-99.
DR PDB; 43C9; 24-JUL-02.
DR PDB; 43CA; 24-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEEA6604A26C3 CRC64;

Query Match 74.2%; Score 432.5; DB 11; Length 107;
Best Local Similarity 77.6%; Pred. No. 1.1e-39;
Matches 83; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

QY 4 MTQSPDSLAVSLGERVTMNCSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTRESG 63
DB 1 MTQSPSSLAMSVGQKVTMCSKSSQSVLSNNTQKNYLAWYQOKPGQSPPELLVYFASTRSG 60
QY 64 VPDRFSGSGSGTDFTLTITSSVQAEADLAVYYCHQ-YLSSYTFGGGTKL 109
DB 61 VPDRFMGSGSGTDFTLTITSSVQTEADLADYFCQCHYRTPFTFGSGTKL 107

RESULT 2

ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homindae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035036; AAD56272.1; -.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; I30601; I30601.
DR PIR; PH0963; PH0963.
DR PIR; PH0965; PH0965.
DR PIR; S34096; S34096.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Ig_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EB197 CRC64;

Query Match 67.1%; Score 391; DB 4; Length 109;
Best Local Similarity 67.3%; Pred. No. 4e-35;
Matches 76; Conservative 18; Mismatches 13; Indels 6; Gaps 2;

QY 1 DIVMTQSPDSLAVSLGERVTMNCSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTR 60
DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSV-----SSSYLAWYQOKPGQAPRLLIYGASSR 55

QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEADLAVYYCHQYLISS-YTFGGGTKLEIK 112
DB 56 ATGIDPRFSGSGSGTDFTLTISRLEPEDCAVYYCQYQSSPLTFGGGTKVEIK 108

RESULT 3

ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homindae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes."
RT J. Immunol. 161:2020-2031(1998).
RL EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Ig_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BH43E9C5B577F16 CRC64;

Query Match 66.7%; Score 389; DB 4; Length 107;
Best Local Similarity 67.0%; Pred. No. 6.5e-35;
Matches 75; Conservative 15; Mismatches 16; Indels 6; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMNCSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTR 60
DB 1 DIQMTQSPSSLASVGDRTVITCRASQSI-----SSYINWYQOKPGKAPKLLIYAASSL 54
QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEADLAVYYCHQYLISSYTFGGGTKLEIK 112
DB 55 QSGVPSRFSGSGSGTDFTLTITSSLPEDFATYYCQYSYTLTFGGGTKVEIK 106

RESULT 4

ID Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.

DR PIR; C32248; C32248.
DR PIR; F32530; F32530.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
DR PIR; PH1044; PH1044.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S24500; S24500.
DR PIR; S24501; S24501.
DR PIR; S24503; S24503.
DR PIR; S24504; S24504.
DR PIR; S24529; S24529.
DR PIR; S24532; S24532.
DR PIR; S24533; S24533.
DR PIR; S24535; S24535.
DR PIR; S24536; S24536.
DR PIR; S24538; S24538.
DR PDB; 1I9I; 25-DEC-02.
DR PDB; 1LO2; 31-JUL-02.
DR PDB; 1LO4; 31-JUL-02.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match	65.7%;	Score 383;	DB 11;	Length 238;
Best Local Similarity	69.0%;	Pred. No. 8.3e-34;		
Matches 78; Conservative	12;	Mismatches 21;	Indels 2;	Gaps 2;

```
QY      1 DVMTQSPDSLAVSLGERTVNMNCKSSQSQSVLYSSNQKNYLAWYOQKPGOSPKLITYASTR    60
        |:|::| | |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     20 DVMTQTPLSLPVSLSGDQASISCRSSQSIIVH-SNGNTYLEWYLQKPGOSPKLITYKYSNR    78
```

```

QY      61  ESGVPDRFSGSGSGTDFTLTISSVQAEDLAVYYCHQYLS-SYTFGGGTGLEIK 112
      |||||
      79  FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGSGTGLEIK 131
Db

```

RESULT 5
09UL70

```

ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1

```

FT	NON TER	108	108
SQ	SEQUENCE	108 AA;	11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match	64.9%;	Score 378.5;	DB 4;	Length 108;
Best Local Similarity	67.3%;	Pred. No. 9.3e-34;		
Matches	76;	Conservative	13;	Mismatches 17;
			Indels	7;
			Gaps	2;

```
QY      1 DIVMTQSPDLSLAVSLGERVTITNCKSSQSIVLYSSNQKNTLAAYQQQPGQSPKLLIYWASTR   60
        ||||| : : : : : : : : : : ||||| : : |||||
Db      1 DIQMGTGSSSLASVGDRTTTCRASQGI-----SNYLAWYQQQPGKVPKSLIIYAASSTL   54
```

```
QY      61  ESGVPDRFSGSGSGTDFTLTITSSVAEDLAVYYCHQYLSS-YTFCGGTKLEIK 112
      : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      55  QSGVPSRFSGSGSGTDFTLTITSLQPEDAVATYYCQKYNAPRTFGPGTKLEIK 107
```

RESULT 6
Q9UL85
ID Q9UL85 PRELIMINARY; PRT; 109 AA.

DE
OS
OC
OC
CX

NCBI_TaxID=9606;

Homo sapiens (Human) .
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus." *J*

RL Clin. Immunol. Immunopathol. 87:184-192 (1998).

DR PIR; D30609; D30609.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

FT	NON_TER	1	-1	
FT	NON_TER	109	109	
SEQ	SEQUENCE	109 AA;	11761 MM;	FB1E43E7C7AFACCC CRC64;

Query Match	64.8%;	Score 378;	DB 4;	Length 109;
Best Local Similarity	67.5%;	Pred. NO. 1.1e-33;		
Matches 77;	Conservative 17;	Mismatches 12;	Indels 8;	Gaps 3;

```
QY      1 DIWMTQSPDLSAVSLGERVTWNCCKSSQSYLYSSNQKNYLAWYQOKPGQSPKLLIYWASTR 60
      :||||| : :| | | : :| | | : :| | | : :| | | : :| | | : :| | |
Db      1 EIVMTQSPATLSVSPGERATLSCWASQSL--SSN---LAWYQOKPGQAPRLIIYGASTR 54
```

QY 61 ESGVPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYL--SYTFGGGKLEIK 112
 ::| | | | | : | | | | : | | | | |
Ddb 55 ATGTPARFSGSGGTFTLTISLSQSEDAFYHCQYNWPPPLTFFGGTKVEIK 108

Q8VCI6	PRELIMINARY;	PRT;	238 AA..
ID Q8VCI6			

AC coverage, 2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Eucleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RESULT 7		
Q8VCI6		
ID	Q8VCI6	PRELIMINARY; PRT; 238 AA.
AC	Q8VCI6;	
DT	01-MAR-2002	(TrEMBLrel. 20, Created)
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)
DE	Hypothetical protein.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	

OK NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -
DR PIR; A27887; A27887.
DR PIR; A32248; A32248.
DR PIR; A33933; A33933.
DR PIR; B27887; B27887.
DR PIR; B30577; B30577.
DR PIR; B31485; B31485.
DR PIR; B32248; B32248.
DR PIR; B41940; B41940.
DR PIR; C27887; C27887.
DR PIR; C32248; C32248.
DR PIR; C34904; C34904.
DR PIR; D27887; D27887.
DR PIR; D29380; D29380.
DR PIR; E28833; E28833.
DR PIR; F32530; F32530.
DR PIR; H31485; H31485.
DR PIR; PH0106; PH0106.
DR PIR; PH1030; PH1030.
DR PIR; PH1031; PH1031.
DR PIR; PH1034; PH1034.
DR PIR; PL0257; PL0257.
DR PIR; PT0359; PT0359.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S26334; S26334.
DR PIR; S53750; S53750.
DR PIR; S60066; S60066.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 64.7%; Score 377; DB 11; Length 238;
Best Local Similarity 67.8%; Pred. No. 3.8e-33;
Matches 78; Conservative 15; Mismatches 16; Indels 6; Gaps 3;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
DB 20 DVVMTQTPLSLPVSLGDQASISCRSSQSLVH-SNGNTYLHWYLOKPGQSPKLLIYKVSNR 78
QY 61 ESGVPPDRFSGSGSGTDFTLTITSSVQAEDLAVYVYCHQYLLSY--TFGGGTKLEIK 112
DB 79 FSGVPPDRFSGSGSGTDFTLTITSSVQAEDLAVYVYCHQYLLSY--STHVPPTFGGGTKLEIK 131

RESULT 8
Q9UL77 PRELIMINARY; PRT; 108 AA.
ID Q9UL77
AC Q9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 64.6%; Score 376.5; DB 4; Length 108;
Best Local Similarity 65.5%; Pred. No. 1.5e-33;
Matches 74; Conservative 16; Mismatches 16; Indels 7; Gaps 2;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
DB 1 DIQMTQSPSLASVGVDRVITCRASQSI-----SSYLNWYQOKPGKAPNLLIYAASSL 54
QY 61 ESGVPPDRFSGSGSGTDFTLTITSSVQAEDLAVYVYCHQ-YLSSYTFGGGTKLEIK 112
DB 55 QSGVPPDRFSGSGSGTDFTLTITSSLPEDFATYVYCCQSYSTSWTFEGGTKVEIK 107

RESULT 9
Q920E9 PRELIMINARY; PRT; 111 AA.
ID Q920E9
AC Q920E9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;

Query Match 64.6%; Score 376.5; DB 11; Length 111;
Best Local Similarity 68.1%; Pred. No. 1.6e-33;
Matches 77; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
DB 1 DIVLTQSPASLAVSLGGRATISCRASKSV--STSGYSYMHWYQOKPGQSPKLLIYLASNL 58
QY 61 ESGVPPDRFSGSGSGTDFTLTITSSVQAEDLAVYVYCHQYLLSYTFGGGTKLEIK 112
DB 59 ESGVPPDRFSGSGSGTDFTLTITSSVQAEDLAVYVYCHQYLLSYTFGGGTKLEIK 111

```
RESULT 10
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID Q9UL81
AC Q9UL81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match
Best Local Similarity 64.5%; Score 376; DB 4; Length 107;
Matches 72; Conservative 16; Mismatches 18; Indels 6; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYMASTR 60
Db 1 DIVMTQSPSSLASVSGDRVTTCRASQSI-----SNYLNWYQOKPGKAPNLLIYAASL 54

QY 61 ESGVPRFSGSGSGTDFLTITSSVQAEDLAVYYCHQYLS-SYTFGGGTLEIK 112
Db 55 QSGVPSRFSGSGSGTDFLTITSLQAEQEDFATYYCCQSYSAITFGPGTKVDIR 106

RESULT 11
Q9UL83 PRELIMINARY; PRT; 108 AA.
ID Q9UL83
AC Q9UL83;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P80362; IWTL.
```

```
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match
Best Local Similarity 63.9%; Score 372.5; DB 4; Length 108;
Matches 76; Conservative 17; Mismatches 13; Indels 7; Gaps 3;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYMASTR 60
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSV--SSN----LAWYQOKPGQAPRLLIYCASTR 54

QY 61 ESGVPRFSGSGSGTDFLTITSSVQAEDLAVYYCHQYLS-SYTFGGGTLEIK 112
Db 55 ATGTPARFSGSGSGTEFTLTITSLQFEDFAVYVQHYNMWPFTFGPGTKVDIK 107

RESULT 12
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79
AC Q9UL79;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match
Best Local Similarity 63.7%; Score 371.5; DB 4; Length 108;
Matches 74; Conservative 14; Mismatches 18; Indels 7; Gaps 2;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYMASTR 60
Db 1 DIVMTQSPSLASVSGDRVTTCRASQSI-----SSYLNWYQOKPGKAPNLLIYAASL 54

QY 61 ESGVPRFSGSGSGTDFLTITSSVQAEDLAVYYCHQYLS-SYTFGGGTLEIK 112
Db 55 QSGVPSRFSGSGSGTDFLTITSLQSEDFATYYCCQYSPFPFTFGGTKEIK 107

RESULT 13
Q8NEKO PRELIMINARY; PRT; 239 AA.
ID Q8NEKO
AC Q8NEKO;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
```

DT 01-OCT-2002 (Tremblrel. 22, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AAH30814.1; -
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40357; S40357.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 63.3%; Score 369; DB 4; Length 239;
Best Local Similarity 67.3%; Pred. No. 2.9e-32;
Matches 76; Conservative 13; Mismatches 22; Indels 2; Gaps 2;

QY 1 DIVMTQSPDLSAVSLGERVTMNCSSQSVLYSSNQKYLAWYQKPGQSPKLLIYMASTR 60
Db 21 DIVMTQSPDLSAVSLGERVTMNCSSQSVLYSSNQKYLAWYQKPGQSPKLLIYMASTR 79

QY 61 ESGVDPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLSS-YTFGGGTKLEIK 112
Db 80 ASGVDPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLSS-YTFGGGTKLEIK 132

RESULT 14

Q9UL86 PRELIMINARY; PRT; 109 AA.

AC Q9UL86;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035028; AAD56264.1; -
DR PIR; B30607; B30607.
DR PIR; I30601; I30601.
DR HSSP; P80362; IWTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 109 109

SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 63.0%; Score 367; DB 4; Length 109;
Best Local Similarity 62.8%; Pred. No. 1.7e-32;
Matches 71; Conservative 20; Mismatches 16; Indels 6; Gaps 2;

QY 1 DIVMTQSPDLSAVSLGERVTMNCSSQSVLYSSNQKYLAWYQKPGQSPKLLIYMASTR 60
Db 1 DIVMTQSPDLSAVSLGERVTMNCSSQSVLYSSNQKYLAWYQKPGQSPKLLIYMASTR 55

QY 61 ESGVDPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLSS-YTFGGGTKLEIK 112
Db 56 ATGIPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLSS-YTFGGGTKLEIK 108

RESULT 15

Q8VC55 PRELIMINARY; PRT; 239 AA.

AC Q8VC55;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021781; AAH21781.1; -
DR PIR; A33933; A33933.
DR PDB; 1KC5; 24-JUL-02.

DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF02950; Conotoxin; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 62.8%; Score 366; DB 11; Length 239;
Best Local Similarity 65.8%; Pred. No. 6.2e-32;
Matches 75; Conservative 18; Mismatches 17; Indels 4; Gaps 3;

QY 1 DIVMTQSPDLSAVSLGERVTMNCSSQSVLYSSNQKYLAWYQKPGQSPKLLIYMASTR 60
Db 21 DIVMTQSPDLSAVSLGERVTMNCSSQSVLYSSNQKYLAWYQKPGQSPKLLIYMASTR 79

QY 61 ESGVDPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQ-YLSSYTFGGGTKLEIK 112
Db 80 FSGVDPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQ-YLSSYTFGGGTKLEIK 132

Search completed: March 26, 2004, 05:07:46
Job time : 35.3688 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 26, 2004, 04:50:40 ; Search time 45.9113 Seconds
(without alignments)
744.658 Million cell updates/sec

Title: US-10-056-052A-20

Perfect score: 647
Sequence: 1 QVQLKESGPGLVKPSQTLST.....YYGYDGFVYWGQGLVTSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647	100.0	121	5 AAE29271	Aae29271 S. aureus
2	605	93.5	121	5 AAE29267	Aae29267 S. aureus
3	538.5	83.2	118	5 AAE29269	Aae29269 S. aureus
4	524.5	81.1	118	5 AAE29265	Aae29265 S. aureus
5	523.5	80.9	118	4 AAB81970	Aab81970 Gangliosid
6	523.5	80.9	581	4 AAB81972	Aab81972 Gangliosid
7	510.5	78.9	118	6 ABJ18564	Abj18564 Gangliosid
8	506	78.2	119	4 AAB69675	Aab69675 Murine mi
9	506	78.2	138	4 AAB69656	Aab69656 Murine mi
10	505	78.1	115	5 AAE29298	Aae29298 S. aureus
11	502	77.6	113	2 AAW23025	Aaw23025 Humanized
12	496	76.7	121	3 AAB10020	Aab10020 H. pylori
13	496	76.7	125	6 ABR44627	Abra44627 Murine va
14	496	76.7	476	4 AAB49243	Aab49243 ChimERIC
15	495	76.5	117	6 ABJ18566	Abj18566 Gangliosid
16	494.5	76.4	137	2 AAW30273	Aaw30273 Heavy cha
17	494	76.4	183	2 AAR15326	Aar15326 Anti-IL2R
18	494	76.4	183	2 AAR32128	Aar32128 Anti-IL2R
19	493	76.2	121	7 ADD25691	Add25691 Binding d
20	493	76.2	271	7 ADD25693	Add25693 Binding d
21	493	76.2	556	2 ADD25707	Add25707 Binding d
22	492.5	76.1	116	2 AAR40951	Aar40951 Mouse ger
23	492	76.0	119	2 AAY49218	Aay49218 Heavy cha
24	492	76.0	119	5 AAU72838	Aau72838 Anti-NKG2
25	492	76.0	119	6 ADA14778	Ada14778 Peptide f

26	492	76.0	119	7 ADC35320	Adc35320 Anti-Idio
27	491.5	76.0	119	3 AAY94215	Aay94215 Murine co
28	491	75.9	241	4 AAB73623	Aab73623 Humanised
29	490	75.7	119	7 ABR63919	Abri63919 Murine C5
30	489.5	75.7	118	4 AAB81973	Aab81973 Gangliosid
31	489.5	75.7	137	4 AAB81975	Aab81975 Gangliosid
32	488.5	75.5	135	1 AAP70991	Aap70991 Sequence
33	488.5	75.5	211	2 AAR56231	Aar56231 Peptide c
34	488	75.4	127	2 AAR06355	Aar06355 Peptide c
35	487.5	75.3	116	4 AAU07513	Aau07513 Antibody
36	487.5	75.3	120	2 AAY22432	Aay22432 TM27 anti
37	487.5	75.3	239	2 AAW09813	Aaw09813 VL1ys-1ln
38	487.5	75.3	239	2 AAW35561	Aaw35561 ECOR1-Hln
39	487.5	75.3	241	2 AAR21261	Aar21261 VHD1.3-Hu
40	487.5	75.3	242	2 AAR06483	Aar06483 18-2-3-/T
41	487.5	75.3	242	2 AAR43680	Aar43680 Single ch
42	487.5	75.3	242	2 AAR99650	Aar99650 Single ch
43	487.5	75.3	267	2 AAR02192	Aar02192 18-2-3/TR
44	487.5	75.3	267	2 AAR04841	Aar04841 Two linke
45	487.5	75.3	272	2 AAR21260	Aar21260 ScFv sequ

ALIGNMENTS

RESULT 1	
AAE29271	standard; protein; 121 AA.
ID	AAE29271; (first entry)
XX	AAE29271;
AC	
XX	
DT	27-JAN-2003
XX	(first entry)
DE	S. aureus ClfA specific monoclonal antibody 12-9VH-Hu protein.
XX	
OS	Staphylococcus aureus.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	31..35
FT	/note= "CDR1"
FT	50..65
FT	/note= "CDR2"
FT	98..110
FT	/note= "CDR3"
XX	
PN	WO200272600-A2.
XX	
PD	19-SEP-2002.
XX	
PF	28-JAN-2002; 2002WO-US002296.
XX	
PR	26-JAN-2001; 2001US-0264072P.
PR	12-MAR-2001; 2001US-0274611P.
PR	18-JUN-2001; 2001US-0298413P.
PR	30-JUL-2001; 2001US-0308116P.
XX	
PA	(INHT-) INHIBITEX INC.
XX	
PI	Patel JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX	
DR	WPI; 2002-759834/82.
DR	N-PSDB; AAD46870.
XX	
PT	New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT	treating or preventing Staphylococcus aureus infection e.g. wound
PT	infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
PT	a human or animal.
XX	
PS	Claim 13; Page 42; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 12-9VH-Hu (humanised variable light sequence) protein
XX
SQ Sequence 121 AA;

Query Match 100.0%; Score 647; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 7.6e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLKESGPGLVKPSQTLITCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGNTDYN 60
Db 1 QVQLKESGPGLVKPSQTLITCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGNTDYN 60

QY 61 SALKSRISISKDNSKNQVFLKMSLTADTAVYYCARKEFFYYGYDGFVYWGQGLVTVS 120
Db 61 SALKSRISISKDNSKNQVFLKMSLTADTAVYYCARKEFFYYGYDGFVYWGQGLVTVS 120

QY 121 S 121
Db 121 S 121

RESULT 2
ID AAE29267 standard; protein; 121 AA.
XX AAE29267;
AC AAE29267;
XX
DT 27-JAN-2003 (first entry)
XX
DE S. aureus ClfA specific monoclonal antibody 12-9VHC-1 protein.
XX
KW Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Region 31..35
FT /note= "CDR1"
FT Region 50..65
FT /note= "CDR2"
FT Region 98..110
FT /note= "CDR3"
XX
PN WO200272600-A2.
XX
PD 19-SEP-2002.
XX
PF 28-JAN-2002; 2002WO-US002296.
XX
PR 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
PR 18-JUN-2001; 2001US-0298413P.
PR 30-JUL-2001; 2001US-0308116P.
XX
PA (INH1-) INHIBITEX INC.
XX
PI Patcl JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
DR WPI: 2002-759834/82.
DR N-PSDB; AAD46866.

XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
PT a human or animal.
XX
PS Claim 13; Page 36; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 12-9VHC-1 (variable heavy sequence) protein
XX
SQ Sequence 121 AA;

Query Match 93.5%; Score 605; DB 5; Length 121;
Best Local Similarity 92.6%; Pred. No. 6.5e-49;
Matches 112; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 QVQLKESGPGLVKPSQTLITCTISGFSLSRYSVHWVRQPPGKLEWLGIMWGNTDYN 60
Db 1 QVQLKESGPGLVAPSQSLITCAISGFSLSRYSVHWVRQPPGKLEWLGIMWGNTDYN 60

QY 61 SALKSRISISKDNSKNQVFLKMSLTADTAVYYCARKEFFYYGYDGFVYWGQGLVTVS 120
Db 61 SALKSRISISKDNSKNQVFLKMSLTQTDITAMYYCARKEFFYYGYDGFVYWGQGLVTVS 120

QY 121 S 121
Db 121 A 121

RESULT 3
ID AAE29269 standard; protein; 118 AA.
XX AAE29269;
AC AAE29269;
XX
DT 27-JAN-2003 (first entry)
XX
DE S. aureus ClfA specific monoclonal antibody 35-220VHC-1 protein.
XX
KW Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Region 31..35
FT /note= "CDR1"
FT Region 50..65
FT /note= "CDR2"
FT Region 98..107
FT /note= "CDR3"
XX
PN WO200272600-A2.
XX
PD 19-SEP-2002.
XX
PF 28-JAN-2002; 2002WO-US002296.
XX
PR 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
PR 18-JUN-2001; 2001US-0298413P.
PR 30-JUL-2001; 2001US-0308116P.

XX (INHI-) INHIBITEX INC.
XX Patcl JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX WPI; 2002-759834/82.
XX N-PSDB; AAD46868.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
XX treating or preventing Staphylococcus aureus infection e.g. wound
XX infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
XX a human or animal.
XX
XX Claim 13; Page 37; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
XX factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
XX monoclonal antibody is useful for treating or preventing S. aureus
XX infection in a human or animal, and for inhibiting the binding of
XX staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
XX S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
XX protein is useful for inducing an immunological response in a human or
XX animal. These staphylococcal infections include wound infections, sepsis,
XX impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
XX present sequence is Staphylococcus aureus ClfA specific monoclonal
XX antibody 35-220VHC-1 (variable heavy sequence) protein
XX
XX Sequence 118 AA;
SQ
Query Match 83.2%; Score 538.5; DB 5; Length 118;
Best Local Similarity 84.3%; Pred. No. 1e-42;
Matches 102; Conservative 6; Mismatches 10; Indels 3; Gaps 1;
QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSISRYSVHWVRQPPGKGLEWLGMIWGGGNTDYN 60
DB 1 QVQLKESGPGLVKPSQSLSTCTVSGFSLRYSVHWVRQPPGKGLEWLGMIWGGGNTDYN 60
QY 61 SALKSRLSISKNSKNQVFLKMNSLTAADTAVYYCARKGEFFYYGYDGFVYWGQGLVTYS 120
DB 61 SALKSRLSITKNSKSKQVFLKMNSLQTDPTAMYCCATA--YYGNSWFAFYWGQGLVTYS 117
QY 121 S 121
DB 118 A 118
RESULT 4
ID AAE29265 standard; protein; 118 AA.
XX
XX AAE29265;
AC
XX
DT 27-JAN-2003 (first entry)
XX
DE S. aureus ClfA specific monoclonal antibody 13-2VHC-3 protein.
XX
XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
XX immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
XX septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH Region 31..35
FT /note= "CDR1"
FT 50..65
FT /note= "CDR2"
FT 98..107
FT /note= "CDR3"
XX
XX WO200272600-A2.
PN
XX
PD 19-SEP-2002.

XX
PF 28-JAN-2002; 2002WO-US002296.
XX
XX 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
PR 18-JUN-2001; 2001US-0298413P.
PR 30-JUL-2001; 2001US-0308116P.
XX
XX (INHI-) INHIBITEX INC.
XX
XX Patcl JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
XX WPI; 2002-759834/82.
XX N-PSDB; AAD46864.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
XX treating or preventing Staphylococcus aureus infection e.g. wound
XX infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
XX a human or animal.
XX
XX Claim 13; Page 35; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
XX factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
XX monoclonal antibody is useful for treating or preventing S. aureus
XX infection in a human or animal, and for inhibiting the binding of
XX staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
XX S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
XX protein is useful for inducing an immunological response in a human or
XX animal. These staphylococcal infections include wound infections, sepsis,
XX impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
XX present sequence is Staphylococcus aureus ClfA specific monoclonal
XX antibody 13-2VHC-3 (variable heavy sequence) protein
XX
XX Sequence 118 AA;
SQ
Query Match 81.1%; Score 524.5; DB 5; Length 118;
Best Local Similarity 81.8%; Pred. No. 2.1e-41;
Matches 99; Conservative 7; Mismatches 12; Indels 3; Gaps 1;
QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSISRYSVHWVRQPPGKGLEWLGMIWGGGNTDYN 60
DB 1 QVHLKESGPGLVKPSQSLSTCTVSGFSLRYSVHWVRQPPGKGLEWLGMIWGGGNTDYN 60
QY 61 SALKSRLSISKNSKNQVFLKMNSLTAADTAVYYCARKGEFFYYGYDGFVYWGQGLVTYS 120
DB 61 SALKSRLSISKNSKSKQVFLKMNSLQTDPTAMYCCA---SAYYGNWFAFYWGQGLVTYS 117
QY 121 S 121
DB 118 A 118
RESULT 5
ID AAB81970 standard; protein; 118 AA.
XX
XX AAB81970;
AC
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD2 specific antibody related protein SEQ ID NO: 13.
XX
XX Ganglioside; GD2; complementation determining region; CDR; antibody;
XX mouse; cancer.
XX
XX Synthetic.
XX
XX WO200123573-A1.
PN
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006773.

XX PR 30-SEP-1999; 99JP-00278290.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX DR WPI; 2001-266163/27.
XX PT Human type complementation-determining domain transplanted antibody and
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of
PT e.g. tumors, has low antigenicity, little side effects but potent
PT activity in cancer.
XX PS Claim 10; Page 102-103; 123pp; Japanese.
XX CC The present invention describes an antibody, which can react specifically
CC with ganglioside GD2, and is transplanted with a human type
CC complementation-determining domain (CDR), or its fragments. The antibody
CC and its derivatives are useful in diagnosis and therapy of tumours,
CC particularly cancer diagnosis. The present sequence is a protein used in
CC the exemplification of the invention
XX XX
SQ Sequence 118 AA;

Query Match 80.9%; Score 523.5; DB 4; Length 118;
Best Local Similarity 80.2%; Pred. No. 2.6e-41;
Matches 97; Conservative 13; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGIMWGNTDYN 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGFSLASYNHWVRQPPGKGLWLGIVWAGGSTNYN 60
QY 61 SALKSRISISKDNSKNQVFLKMSLTADTAVYYCAKRGFFYYGYDGFVYWGQGLTVTS 120
DB 61 SALKSRITISKDNSKNQVFLKMSLTADTAVYYCAKRSD---DYSWFAFWGQGLTVTS 117
QY 121 S 121
DB 118 S 118

RESULT 6
AAB81972
ID AAB81972 standard; protein; 581 AA.
XX AC AAB81972;
XX DT 03-JUL-2001 (first entry)
XX DE Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
XX KW Ganglioside; GD2; complementation determining region; CDR; antibody;
KM mouse; cancer.
XX OS Synthetic.
XX PN WO200123573-A1.
XX PD 05-APR-2001.
XX PF 29-SEP-2000; 2000WO-JP006773.
XX PR 30-SEP-1999; 99JP-00278290.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX DR WPI; 2001-266163/27.
PT Human type complementation-determining domain transplanted antibody and
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of

PT e.g. tumors, has low antigenicity, little side effects but potent
PT activity in cancer.
XX PS Example 3; Page 111-114; 123pp; Japanese.
XX CC The present invention describes an antibody, which can react specifically
CC with ganglioside GD2, and is transplanted with a human type
CC complementation-determining domain (CDR), or its fragments. The antibody
CC and its derivatives are useful in diagnosis and therapy of tumours,
CC particularly cancer diagnosis. The present sequence is a protein used in
CC the exemplification of the invention
XX XX
SQ Sequence 581 AA;

Query Match 80.9%; Score 523.5; DB 4; Length 581;
Best Local Similarity 80.2%; Pred. No. 1.6e-40;
Matches 97; Conservative 13; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLSTCTISGFSLSRYSVHWVRQPPGKGLWLGIMWGNTDYN 60
DB 1 QVQLQESGPGLVKPSQTLSTCTVSGFSLASYNHWVRQPPGKGLWLGIVWAGGSTNYN 60
QY 61 SALKSRISISKDNSKNQVFLKMSLTADTAVYYCAKRGFFYYGYDGFVYWGQGLTVTS 120
DB 61 SALKSRITISKDNSKNQVFLKMSLTADTAVYYCAKRSD---DYSWFAFWGQGLTVTS 117
QY 121 S 121
DB 118 S 118

RESULT 7
ABJ18564
ID ABJ18564 standard; protein; 118 AA.
XX AC ABJ18564;
XX DT 18-FEB-2003 (first entry)
XX DE Ganglioside-associated recombinant antibody related VH3 P3 protein.
XX KW Cytostatic; chimeric antibody; monoclonal antibody; ECACC 94113026;
KM N-glycosylated ganglioside; anti-idiotypic monoclonal 1E10; metastatic;
KM breast cancer; melanoma; tumour; lung; digestive; urogenital tract;
KM sarcoma; neuroectodermal.
XX OS Unidentified.
XX PN WO200281496-A2.
XX PD 17-OCT-2002.
XX PF 08-APR-2002; 2002WO-CU0000003.
XX PR 06-APR-2001; 2001CU-00000084.
XX PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
PA (DRIO/) MATEO DE ACOSTA DEL RIO C M.
PA (VALL/) LOMBARDERO VALLADARES J.
PA (NABA/) ROQUE NAVARRO L T.
PA (REQU/) LOPEZ REQUENA A.
XX PI Mateo De Acosta Del Rio CM, Lombardero Valladares J;
PI Roque Navarro LT, Lopez Requena A;
XX DR WPI; 2003-046857/04.
XX DR N-PSDB; ABT14038.
XX PT New chimeric antibodies, useful for treatment, prevention and diagnosis
PT of tumors that express gangliosides, are derived from monoclonal
PT antibodies P3 or 1E10.
XX PS Example 6; Fig 1; 31pp; Spanish.

XX The invention relates to a chimeric antibody, derived from a monoclonal
CC antibody, which recognises N-glycosylated gangliosides and is produced by
CC hybridoma ECACC 9413026. The chimeric antibody, and similar antibodies
CC derived from the anti-idiotypic monoclonal 1B10 (recognising P3) are used
CC for treatment, localisation and in vivo identification of breast cancer
CC and melanoma, their metastases and relapses, tumours of lung, digestive
CC and urogenital tracts, and sarcoma and tumours of neuroectodermal origin.
CC This sequence represents a protein relating to the chimeric antibody of
CC the invention

XX Sequence 118 AA;

CC donor and human immunoglobulin and producing a combined antibody which
CC contains part of each. These are useful in the treatment of graft-versus-
CC host disease, transplant rejection, autoimmune diseases such as diabetes,
CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic
CC lupus erythematosus, herpes infections, CMV virus infections and myeloid
CC leukaemia. The present sequence is an antibody used to demonstrate the
CC method of the invention

XX Sequence 119 AA;

Query Match 78.9%; Score 510.5; DB 6; Length 118;
Best Local Similarity 81.1%; Pred. No. 4.3e-40;
Matches 99; Conservative 6; Mismatches 8; Indels 9; Gaps 2;

QY 1 QVQLKESGPGLVKPSQTLISITCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGNTDYN 60
Db 1 QVQLKESGPGLVAPSQSLISITCTVSGFSLSRYSVHWVRQPPGKGLEWLGMIWGGSTDYN 60
QY 61 SALKSRLSISKDNSKQVFLKMNSLTAADTAIVYYCARKGEFYYGYDG-----FVYWGQGT 115
Db 61 SALKSRLSISKDNSKQVFLKMNSLQTDPTAIVYYCARSGV---REGRAQAWFAVWGQGT 116
QY 116 LV 117
Db 117 LV 118

RESULT 8
AAB69675
ID AAB69675 standard; protein, 119 AA.

XX AC AAB69675;

DT 30-APR-2001 (first entry)

XX Murine mik-betal antibody heavy chain SEQ ID NO: 60.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
KW light chain; graft versus host disease; transplant; autoimmune disease;
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.

PN US6180370-B1.

PD 30-JAN-2001.

PF 07-JUN-1995; 95US-00484537.

PR 28-DEC-1988; 88US-00290975.

PR 13-FEB-1989; 89US-00310252.

PR 28-SEP-1990; 90US-00590274.

PR 19-DEC-1990; 90US-00634278.

PA (PROT-) PROTEIN DESIGN LABS INC.

PI Queen CL, Selick HE;

DR WPI; 2001-190856/19.

PT Producing humanized immunoglobulin, involves producing a cell containing
PT DNA segments encoding humanized heavy and light chain variable regions,
PT and expressing the DNA segments in the cell.

PS Disclosure; Fig 5; 145pp; English.

XX The present invention describes a method of producing humanised
CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
CC humanised version of an immunoglobulin. This is obtained by comparing a

Query Match 78.2%; Score 506; DB 4; Length 119;
Best Local Similarity 75.2%; Pred. No. 1.2e-39;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGLVKPSQTLISITCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGNTDYN 60
Db 1 QVQLKESGPGLVQPSQSLISITCTVSGFVSIVYGVHWIRQSPGKGLEWLGVIWGGSTDYN 60
QY 61 SALKSRLSISKDNSKQVFLKMNSLTAADTAIVYYCARKGEFYYGYDGFVYWGQGLTVTS 120
Db 61 AAFISRLTISKDNSKQVFFKVNSLQPADTAIVYYCARAGD--YNYDGFAYWGQGLTVTS 118
QY 121 S 121
Db 119 A 119

RESULT 9
AAB69656
ID AAB69656 standard; protein, 138 AA.

XX AC AAB69656;

DT 30-APR-2001 (first entry)

XX Murine mik-betal antibody heavy chain SEQ ID NO: 33.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
KW light chain; graft versus host disease; transplant; autoimmune disease;
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.

PN US6180370-B1.

PD 30-JAN-2001.

PF 07-JUN-1995; 95US-00484537.

PR 28-DEC-1988; 88US-00290975.

PR 13-FEB-1989; 89US-00310252.

PR 28-SEP-1990; 90US-00590274.

PR 19-DEC-1990; 90US-00634278.

PA (PROT-) PROTEIN DESIGN LABS INC.

PI Queen CL, Selick HE;

DR WPI; 2001-190856/19.

DR N-PSDB; AAF58728.

PT Producing humanized immunoglobulin, involves producing a cell containing
PT DNA segments encoding humanized heavy and light chain variable regions,
PT and expressing the DNA segments in the cell.

PS Example 5; Fig 23; 145pp; English.

XX The present invention describes a method of producing humanised
CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
CC humanised version of an immunoglobulin. This is obtained by comparing a
CC donor and human immunoglobulin and producing a combined antibody which
CC contains part of each. These are useful in the treatment of graft-versus-

CC host disease, transplant rejection, autoimmune diseases such as diabetes,
CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic
CC lupus erythematosus, herpes infections, CMV virus infections and myeloid
CC leukaemia. The present sequence is an antibody used to demonstrate the
CC method of the invention

XX Sequence 138 AA;

Query Match 78.2%; Score 506; DB 4; Length 138;
Best Local Similarity 75.2%; Pred. No. 1.4e-39;
Matches 91; Conservative 16; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLKESGPGLVKPSQITISITCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGSNTDYN 60
Db 20 QVQLKQSGPGLVQPSQSISITCTVSGFSVTSYGVMIRQSPGKGLEWLGMIWGGSNTDYN 79
QY 61 SALKSRLSISKDNSKQVFLKMNLSLTADTAVYYCARKEGFYYGYDGFYWGQGLTVTS 120
Db 80 AAFISRLTISKDNSKQVFLKMNLSLTADTAVYYCARAGD--YNYDGFAYWGQGLTVTS 137
QY 121 S 121
Db 138 A 138

RESULT 10
AAE29298
ID AAE29298 standard; protein; 115 AA.

XX AAE29298;
DT 27-JAN-2003 (first entry)

DE S. aureus ClfA specific monoclonal antibody 35-006VHC-1 protein.

XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
XX septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

OS Staphylococcus aureus.

XX Key Location/Qualifiers
FH Region 31..35
FT /note= "CDR1"
FT 50..65
FT /note= "CDR2"
FT 98..104
FT Region /note= "CDR3"

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US002296.

XX 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
PR 18-JUN-2001; 2001US-0298413P.
PR 30-JUL-2001; 2001US-0308116P.

XX (INH1-) INHIBITEX INC.

XX Patli JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX WPI; 2002-759834/82.

XX N-PSDB; AAD46964.

XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
PT a human or animal.

XX Example 7; Page 39; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 35-006VHC-1 (variable heavy sequence) protein

XX Sequence 115 AA;

Query Match 78.1%; Score 505; DB 5; Length 115;
Best Local Similarity 81.0%; Pred. No. 1.4e-39;
Matches 98; Conservative 8; Mismatches 9; Indels 6; Gaps 2;

QY 1 QVQLKESGPGLVKPSQITISITCTISGFSLSRYSVHWVRQPPGKGLEWLGMIWGGSNTDYN 60
Db 1 QVQLKESGPGLVAPSQISITCTVSGFSLSRYSVHWVRQPPGKGLEWLGMIWGGSNTDYN 60
QY 61 SALKSRLSISKDNSKQVFLKMNLSLTADTAVYYCARKEGFYYGYDGFYWGQGLTVTS 120
Db 61 SALKSRLNISKDNSKQVFLKMNLSLTQDDTAVYYCARR--LWY---FDVWGAGTTVTS 114
QY 121 S 121
Db 115 S 115

RESULT 11
AAW23025
ID AAW23025 standard; protein; 113 AA.

XX AAW23025;

XX 17-OCT-2003 (revised)
DT 23-MAR-1998 (first entry)

DE Humanized 5D12 monoclonal antibody heavy chain variable region.

XX Human; B7 antigen; CD40; monoclonal antibody; B cell; growth;
KW differentiation; allergy; autoimmune disease.

XX Mus sp.
OS Homo sapiens.
OS Chimeric.

XX WO9731025-A1.

XX 28-AUG-1997.

XX 21-FEB-1997; 97WO-US002858.

XX 23-FEB-1996; 96US-00606293.

XX (CHIR) CHIRON CORP.

XX De Boer M;

XX WPI; 1997-435094/40.

XX N-PSDB; AAT79192.

XX Humanised monoclonal antibody binding CD40 antigen on B cells - to
PT prevent their growth and differentiation, useful to treat or prevent
PT antibody mediated allergies and autoimmune diseases.

XX Example 8; Fig 12; 64pp; English.

XX A novel humanised monoclonal antibody (MAb) has been developed which: (a)
CC binds a human CD40 antigen on the surface of a B cell, to prevent its

CC growth and differentiation; and (b) has an effective number of exposed
CC amino acids in its framework regions that are consistent with amino acid
CC residues found in the corresponding framework regions of a human Ab to
CC provide a reduced immunogenicity in humans. The present sequence
CC represents humanized 5D12 monoclonal antibody heavy chain variable
CC region, used in an example of the present invention. The Mab can be used
CC to prevent or treat antibody mediated diseases, particularly
CC immunoglobulin E (IgE) mediated allergies, systemic lupus erythematosus,
CC primary biliary cirrhosis, idiopathic thrombocytopenia purpura and
CC rheumatoid arthritis. The Mab inhibits the normal B cell response to CD40
CC ligands at relatively low concentrations and is unlikely to cause any
CC immune response in humans. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 113 AA;

Query Match 77.6%; Score 502; DB 2; Length 113;
Best Local Similarity 81.0%; Pred. No. 2.6e-39;
Matches 98; Conservative 7; Mismatches 8; Indels 8; Gaps 2;

QY 1 QVQLKESGPGELVPSQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDYN 60
Db 1 QVQLVESGPGELVPSQSLSTCTVSGFSLRSYVWVRQPPGKLEWLGMMWGGSTDYN 60
QY 61 SALKSRSLISKDNSKNQVFLKNSLTADTAIVYVCARKGEFYGYDGFVYWGQGITVTS 120
Db 61 SALKSRSLISKDNSKNQVFLKNSLTADTAIVYVCARKGEFYGYDGFVYWGQGITVTS 112
QY 121 S 121
Db 113 S 113

RESULT 12
AAB10020
ID AAB10020 standard; protein; 121 AA.
XX
AC AAB10020;
XX
DT 01-NOV-2000 (first entry)
XX
DE H. pylori HSP60-binding antibody heavy chain protein.
XX
KM Acid-resistant microorganism; detection; faecal; intestine; infection;
KM monoclonal antibody; heat shock protein; HSP60; heavy chain.
XX
OS Unidentified.
XX
PN WO200026671-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-EP008212.
XX
PR 29-OCT-1998; 98EP-00120517.
PR 06-NOV-1998; 98EP-00120687.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
PI Ringels A;
XX
DR WPI; 2000-365747/31.
DR N-PSDB; AAA40200.
XX
XX
PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
PT pylori, comprises reacting a fecal sample with two binding reagents for
PT antigens that survive intestinal passage.
XX
PS Disclosure; Fig 2; 84pp; German.
XX
CC This invention describes a novel method for the detection of a mammalian
CC infection by an acid-resistant microorganism (A) by treating a faecal

CC sample with at least two different monoclonal antibodies (Mab) (or their
CC fragments or derivatives) or aptamers (collectively (I)) and detecting
CC formation of a complex (C) between (I) and the corresponding antigen of
CC (A). The first and second (I) bind to epitopes of different antigens
CC (Ag). These epitopes are present, after passage through the intestines,
CC in at least some mammals, and have either: (i) their native structure; or
CC (ii) a structure against which an antibody is produced by an animal
CC infected or immunized with (A), or its extract, lysate, derived protein
CC or fragment, or with a synthetic peptide. Practically all mammals display
CC at least one of the specified epitopes. The method is used to detect
CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.
CC tuberculosis, C. jejuni and C. pylori. (I) may also be used
CC therapeutically. The method is direct and non-invasive, and provides an
CC inexpensive and easily standardizable diagnosis, despite possible
CC degradation of antigens during passage through the intestines. This
CC sequence represents the H. pylori heat shock protein, HSP60-binding
CC antibody (DMS ACC2356) heavy chain which is used to illustrate the method
CC of the invention
XX
SQ Sequence 121 AA;

Query Match 76.7%; Score 496; DB 3; Length 121;
Best Local Similarity 79.7%; Pred. No. 1e-38;
Matches 98; Conservative 8; Mismatches 13; Indels 4; Gaps 3;

QY 1 QVQ-LKESGPGELVPSQTLSTCTISGFSLSRYSVHWVRQPPGKLEWLGMIWGGNTDY 59
Db 1 EVQLLESQPGELVAPSQSLSTCTVSGFSLRSYVHWVRQPPGKLEWLGMIWGGSTDY 60
QY 60 NSALKSRSLISKDNSKNQVFLKNSLTADTAIVYVCARK-GEFYGYDGFVYWGQGITV 118
Db 61 NSGLKSRSLISNDNSKSKQVFLKNSLTQDDTAIYVCARKNGGRYPDY--FDYWGQGITV 118
QY 119 VSS 121
Db 119 VSS 121

RESULT 13
ABR44627
ID ABR44627 standard; protein; 125 AA.
XX
AC ABR44627;
XX
DT 25-JUL-2003 (first entry)
XX
DE Murine variable heavy chain amino acid sequence MUVHIB.
XX
KM Mouse; murine; antibody; skin disorder; binding agent; PSMA; cyrostatic;
KM Prostate specific membrane antigen; antipsoriatic; antiarthritic;
KM dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
KM epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
XX
XX Mus musculus.
OS Synthetic.
OS
XX
PN WO2003024388-A2.
XX
PD 27-MAR-2003.
XX
PF 30-MAY-2002; 2002WO-US017204.
XX
PR 20-SEP-2001; 2001US-0324100P.
PR 08-MAR-2002; 2002US-0362612P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Bander N;
XX
DR WPI; 2003-313319/30.
XX

PI Mateo De Acosta Del Rio CM, Lombardero Valladares J;
PI Roque Navarro LT, Lopez Requena A;
XX
DR WPI; 2003-046857/04.

XX New chimeric antibodies, useful for treatment, prevention and diagnosis
PT of tumors that express gangliosides, are derived from monoclonal
PT antibodies P3 or IE10.

XX
PS Example 6; Fig 3; 31pp; Spanish.

XX
CC The invention relates to a chimeric antibody, derived from a monoclonal
CC antibody, which recognises N-glycosylated gangliosides and is produced by
CC hybridoma ECACC 94113026. The chimeric antibody, and similar antibodies
CC derived from the anti-idiotypic monoclonal IE10 (recognising P3) are used
CC for treatment, localisation and in vivo identification of breast cancer
CC and melanoma, their metastases and relapses, tumours of lung, digestive
CC and urogenital tracts, and sarcoma and tumours of neuroectodermal origin.
CC This sequence represents a protein relating to the chimeric antibody of
CC the invention

XX
SQ Sequence 117 AA;

Query Match 76.5%; Score 495; DB 6; Length 117;
Best Local Similarity 80.3%; Pred. No. 1.2e-38;
Matches 98; Conservative 6; Mismatches 8; Indels 10; Gaps 3;

QY 1 QVQLKESGPGLVKPSQTLTITCTISGFSLSRYSVHWVRQPPGKGLVWLGMWGGNTDYN 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLKESGPGLVAPSQSLTITCTVSGFSLSRYSVHWVRQPPGKGLVWLGMWGGSTDYN 60

QY 61 SALKSRLSISKDNSKNQVFLKNSLTAAADTAVYYCARKEFYGYDG----FVYWGQGT 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SALKSRLSISKDNSKQVFLKNSLTQDDTAMYYCARSGV---REGRAQAWFAYWG-GT 115

QY 116 LV 117
||
Db 116 LV 117

Search completed: March 26, 2004, 05:04:04
Job time : 50.913 secs

XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 12-9VL-Hu (humanised variable light sequence) protein
XX
SQ Sequence 112 AA;

Query Match 100.0%; Score 583; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.9e-42;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 DIVMTQSPDLSIAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTR 60
112
DB 1 DIVMTQSPDLSIAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTR 60
QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLLSYTFGGGTKLEIK 112
61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLLSYTFGGGTKLEIK 112
DB 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLLSYTFGGGTKLEIK 112

RESULT 2
AAE29266
ID AAE29266 standard; protein; 112 AA.
XX
AC AAE29266;
XX
DT 27-JAN-2003 (first entry)
XX
DE S. aureus ClfA specific monoclonal antibody 12-9VLA-1 protein.

XX Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX
OS Staphylococcus aureus.

XX Key Location/Qualifiers
FH Region 24. .40
FT /note= "CDR1"
FT Region 56. .62
FT /note= "CDR2"
FT Region 95. .102
FT /note= "CDR3"
XX
PN WO200272600-A2.

XX 19-SEP-2002.
PD
XX 28-JAN-2002; 2002WO-US002296.
PF
XX 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
PR 18-JUN-2001; 2001US-0298413P.
PR 30-JUL-2001; 2001US-0308116P.

XX (INH-1) INHIBITEX INC.

XX Patil JM, Hutchins JT, Domanski P, Patel P, Hall A;

DR WPI; 2002-759834/82.

DR N-PSDB; AAD46865.

PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in

PT a human or animal.

PS Claim 11; Page 35; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 12-9VLA-1 (variable light sequence) protein
XX
SQ Sequence 112 AA;

Query Match 94.9%; Score 553; DB 5; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.7e-39;
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DY 1 DIVMTQSPDLSIAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTR 60
112
DB 1 NIMMTQSPDLSIAVSAAGEKVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTR 60
QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLLSYTFGGGTKLEIK 112
61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLLSYTFGGGTKLEIK 112
DB 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLLSYTFGGGTKLEIK 112

RESULT 3
AAR54933
ID AAR54933 standard; peptide; 112 AA.
XX
AC AAR54933;
XX
DT 25-MAR-2003 (revised)
DT 19-OCT-1994 (first entry)
XX
DE MAb 022 VK chain.

XX Fc receptor; FcR; humanized antibody; hAb; IgG; cancer; allergy;
KW autoimmune disease; heteroantibody; bifunctional antibody; immunotoxin;
KW CDR; complementarity determining region; VH; heavy chain variable region;
KW VK; kappa chain variable region; mononuclear phagocyte; PCR;
KW polymerase chain reaction; primer; site-directed mutagenesis;
KW monoclonal antibody; MAb.

OS Mus sp.

PN WO9410332-A1.

XX 11-MAY-1994.

PF 04-NOV-1993; 93WO-US010384.

PR 04-NOV-1992; 92GB-00023377.

PA (MEDA-) MEDAREX INC.

PI Tempest PR, Harris WJ, Carr FJ;

DR WPI; 1994-167486/20.

XX New humanised antibodies to Fc receptors - used for diagnosis or for
PT treatment of e.g. cancer, allergies and infectious and auto-immune
PT diseases.

PS Disclosure; Page 23; 36pp; English.

XX Humanized antibodies (hAbs) for IgG Fc receptors on human phagocytes
CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma 022WCL-

CC 1), VH chains from human Igs NEMW or KOL, and VK chains from Ig REI.
CC Sequences are provided for mouse 022 VH (AAR54931), humanized NEMW-based
CC VH (022 NMYH, AAR54929), humanized KOL-based VH (022 KL VH, AAR54930),
CC mouse 022 VK (AAR54933) and humanized REI-based VK (022 HuVK, AAR54932).
CC during hab production, VH and VK CDNA's were PCR amplified using primers
CC given in AAQ65378-87. Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was
CC performed using oligos AAQ65388-89. The habs can be used in
CC heteroantibody, bifunctional antibody and immunotoxin production.
CC (Updated on 25-MAR-2003 to correct FN field.)
XX

CC Sequence 112 AA;

Query Match 94.5%; Score 551; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 2.5e-39;
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 DIVMTQSPDLSAVSLGERVTNCKSSQSVLYSSNQKNTLAWYQQKPGQSPKLLITWASTR 60
Db 1 NIVMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNTLAWYQQKPGQSPKLLITWASTR 60
OY 61 ESGVDPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLSSTFGGKTLEIK 112
Db 61 ESGVDPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLSSTFGGKTLEIK 112

RESULT 4

AAE29264
ID AAE29264 standard; protein; 112 AA.

XX AAE29264;

DT 27-JAN-2003 (first entry)

XX S. aureus ClfA specific monoclonal antibody 13-2VLA-1 protein.

DE Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KM septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

XX Staphylococcus aureus.

XX Key Location/Qualifiers
FH Region 24..40
FT /note= "CDR1"
FT 56..62
FT /note= "CDR2"
FT 95..102
FT /note= "CDR3"

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US002296.

XX 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
PR 18-JUN-2001; 2001US-0298413P.
PR 30-JUL-2001; 2001US-0308116P.

XX (INH1-) INHIBITEX INC.

XX Patci JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX WPI; 2002-759834/82.
DR N-PSDB; AAD46863.

PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
PT a human or animal.

PS Claim 11; Page 34; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 13-2VLA-1 (variable light sequence) protein

XX Sequence 112 AA;

Query Match 93.5%; Score 545; DB 5; Length 112;
Best Local Similarity 92.0%; Pred. No. 8.1e-39;
Matches 103; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 1 DIVMTQSPDLSAVSLGERVTNCKSSQSVLYSSNQKNTLAWYQQKPGQSPKLLITWASTR 60
Db 1 NIVMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNTLAWYQQKPGQSPKLLITWASTR 60
OY 61 ESGVDPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLSSTFGGKTLEIK 112
Db 61 ESGVDPDRFSGSGGTDFLTITSSVQAEDLAVYYCHQYLSSTFGGKTLEIK 112

RESULT 5

AAE29268
ID AAE29268 standard; protein; 112 AA.

XX AAE29268;

DT 27-JAN-2003 (first entry)

XX S. aureus ClfA specific monoclonal antibody 35-220VLD-4 protein.

DE Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KM septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

XX Staphylococcus aureus.

XX Key Location/Qualifiers
FH Region 24..40
FT /note= "CDR1"
FT 56..62
FT /note= "CDR2"
FT 95..102
FT /note= "CDR3"

XX WO200272600-A2.

XX 19-SEP-2002.

XX 28-JAN-2002; 2002WO-US002296.

XX 26-JAN-2001; 2001US-0264072P.
PR 12-MAR-2001; 2001US-0274611P.
PR 18-JUN-2001; 2001US-0298413P.
PR 30-JUL-2001; 2001US-0308116P.

XX (INH1-) INHIBITEX INC.

XX Patci JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX WPI; 2002-759834/82.
DR N-PSDB; AAD46867.

PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in

PT a human or animal.
XX
PS Claim 11; Page 37; 80pp; English.
XX
CC The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 35-220VLD-4 (variable light sequence) protein
XX
SQ Sequence 112 AA;

Query Match 93.3%; Score 544; DB 5; Length 112;
Best Local Similarity 92.0%; Pred. No. 9.9e-39;
Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSI... 60
Db 1 NIMMTQSPSS... 60
QY 61 ESGVDPDRFSGSGGT... 112
Db 61 ESGVDPDRFSGSGGT... 112

RESULT 6
ADB97820
ID ADB97820 standard; protein; 113 AA.
XX
AC ADB97820;
XX
DT 04-DEC-2003 (first entry)
XX
DE HEV related protein #SEQ ID 14.
XX
KM Hepatitis E virus; HEV; virucide; vaccine; monoclonal antibody; NE2;
XX
KW infection.
XX
OS Unidentified.
XX
PN WO2003040187-A1.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-CN000797.
XX
PR 08-NOV-2001; 2001CN-00134643.
XX
PA (YANG-) YANG SHENG TANG CO LTD.
XX
PI Xia N, Zhang J, Gu Y, Li S, Ge S, He Z;
XX
DR WPI; 2003-441530/41.
XX
PT Hepatitis E virus monoclonal antibodies and their active fragments, for
PT use in diagnosis and developing remedies e.g. vaccines for preventing or
PT treating hepatitis E virus infection.
XX
PS Claim 2; Page 141; 165pp; Chinese.
XX
CC The invention relates to a monoclonal antibody that binds specifically to
CC hepatitis E virus open-reading frame (ORF) 2. Also disclosed are
CC nucleotide sequences encoding the heavy-chain and/or light-chain variable
CC region of their degeneration sequences. The monoclonal antibody is
CC selected from anti-HEV monoclonal antibody 8C11 secreted by hybridoma
CC CCTCC-C200116, anti-HEV monoclonal antibody 13D8 secreted by hybridoma
CC CCTCC-C200114, anti-HEV monoclonal antibody 8H3 secreted by hybridoma

CC CCTCC-C200117, and anti-HEV monoclonal antibody 16D7 secreted by
CC hybridoma CCTCC-C200114. The monoclonal antibodies and their active
CC fragments are useful in diagnosis and developing remedies e.g. vaccines
CC for preventing or treating hepatitis E virus infection. From the whole
CC HEV gene obtained in patients, the HEV ORF fragment was prepared by using
CC the method of Aye et al. The polypeptide NE2 was then expressed and
CC isolated after biotechnological manipulations, which was characterised.
CC Its analogs were also produced for immunising mice and construction of
CC hybridomas. Tests were carried out to confirm usefulness of such
CC polypeptides and monoclonal antibodies. The current sequence represents a
CC HEV related protein.
XX
SQ Sequence 113 AA;

Query Match 92.8%; Score 541; DB 7; Length 113;
Best Local Similarity 91.1%; Pred. No. 1.8e-38;
Matches 102; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSI... 60
Db 1 NIMMTQSPSS... 60
QY 61 ESGVDPDRFSGSGGT... 112
Db 61 ESGVDPDRFSGSGGT... 112

RESULT 7
AAW90226
ID AAW90226 standard; protein; 263 AA.
XX
AC AAW90226;
XX
DT 10-MAY-1999 (first entry)
XX
DE Anti-B7.2 monospecific triabody 1G10.
XX
DE B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
XX
KW T cell activation; inhibitor; graft versus host disease;
XX
KW transplant rejection; allograft rejection; autoimmune disease; allergy;
XX
KM therapy; human; triabody; antibody; 1G10.
XX
OS Mus sp.
XX
OS Synthetic.
XX
OS Chimeric.
XX
FH Key
FH Peptide
FH Region
FH Peptide
FH Peptide
FT Location/Qualifiers
FT 1..24
FT /note= "pe1B signal peptide"
FT 25..144
FT /note= "anti B7.2 Mab VH region"
FT 145..257
FT /note= "anti B7.2 Mab VL region"
FT 258..263
FT /note= "His6 tag"
XX
PN WO9858965-A2.
XX
PD 30-DEC-1998.
XX
PF 22-JUN-1998; 98WO-EP003791.
XX
PR 20-JUN-1997; 97EP-00870092.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Lorre K, Sablon E, Buysse M, Bosman A;
XX
DR WPI; 1999-105615/09.
XX
DR N-PSDB; AAX01660.
XX
PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection.

XX Example 7.3; Fig 34; 182pp; English.

PS This polypeptide comprises a 1G10 monospecific triabody composed of the

XX CC VH region of anti-B7.2 monoclonal antibody (Mab) 1G10 joined to the VL

CC region of 1G10. A triabody is a mono- a bi- or a trispecific molecule

CC recognising simultaneously e.g. two B7.2 and one B7.1 molecules. It has

CC a rigid structure that prevents simultaneous binding to the 3 targets.

CC Each antigen-binding site is formed by pairing of one VH and one VL

CC domain from the same or from two different polypeptides. The invention

CC relates to novel molecules, including triabodies, which can cross-link

CC and/or cross-react with the costimulatory molecules B7.1 and B7.2

CC expressed on professional antigen-presenting cells, leading to the

CC inhibition of antigen-specific T cell activation. Methods are provided

CC for the production of such B7-binding molecules, and for their use in the

CC treatment or prevention of diseases of the immune system, in particular

CC graft rejection, graft versus host disease, allergy and autoimmune

CC diseases (claimed)

XX

SQ Sequence 263 AA;

Query Match 92.6%; Score 540; DB 2; Length 263;

Best Local Similarity 92.0%; Pred. No. 5e-38;

Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNQKNYLAHYQKPGQSPKLLIYMASTR 60

145 DIELTQSPSSLAVSAGEEVTMTCKSSQSVLYSSNQKNYLAHYQKPGQSPKLLIYMASTR 204

QY 61 ESGVPDRFSGSGGTDTFTLTITSSVQAEDLAVYYCHQYLLSSYTFGGGTKLEIK 112

205 ESGVPDRFSGSGGTDTFTLTITSSVQAEDLAVYYCHQYLLSSYTFGGGTKLEIK 256

Db

RESULT 8

AAW90222

ID AAW90222 standard; protein; 268 AA.

XX

AC AAW90222;

XX

DT 10-MAY-1999 (first entry)

XX

DE Anti-B7.2 monospecific diabody 1G-10.

XX

KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;

KW T cell activation; inhibitor; graft versus host disease;

KW transplant rejection; allograft rejection; autoimmune disease; allergy;

KW therapy; human; diabody; antibody; 1G-10.

XX

OS Mus sp.

OS Synthetic.

OS Chimeric.

OS

XX

FH Key

FT Peptide

FT 1..24

FT /note= "pelB signal peptide"

FT 25..144

FT /note= "anti B7.2 Mab VH region"

FT 145..149

FT /note= "G4S flexible linker"

FT 150..262

FT /note= "anti B7.2 Mab VL region"

FT 263..268

FT /note= "His6 tag"

FT Peptide

XX

XX WO9858965-A2.

XX

PD 30-DEC-1998.

XX

XX

PF 22-JUN-1998; 98WO-EP003791.

XX

PR 20-JUN-1997; 97EP-00870092.

XX

PA (INNO-) INNOGENETICS NV.

XX

PI Lorre K, Sablon E, Buysse M, Bosman A;

XX

DR WPI; 1999-105615/09.

DR N-PSDB; AAX01656.

XX

PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat

PT immune diseases including allograft rejection.

XX

PS Example 7.2; Fig 26; 182pp; English.

XX

XX This polypeptide comprises a 1G-10 monospecific diabody composed of the

CC VH region of anti-B7.2 monoclonal antibody (Mab) 1G-10 joined via a

CC short, flexible linker to the VL region of 1G-10. Mono- or bispecific

CC bivalent molecules are generated by shortening the flexible linker

CC sequence between the VH and VL of the anti-B7.1 scFv B7-24, the anti-B7.2

CC scFv 1G10 and the scFv molecule with dual specificity for B7.1 and B7.2

CC (B7.12) to 5-10 residues, and for bispecific molecules by cross-pairing

CC the VH and VL domains from the 2 scFvs with different antigen recognition

CC (B7.1/B7.2 and B7.12/B7.12). The invention relates to novel molecules,

CC including diabodies, which can cross-link and/or cross-react with the

CC costimulatory molecules B7.1 and B7.2 expressed on professional antigen-

CC presenting cells, leading to the inhibition of antigen-specific T cell

CC activation. Methods are provided for the production of such B7-binding

CC molecules, and for their use in the treatment or prevention of diseases

CC of the immune system, in particular graft rejection, graft versus host

CC disease, allergy and autoimmune diseases (claimed)

XX

SQ Sequence 268 AA;

Query Match 92.6%; Score 540; DB 2; Length 268;

Best Local Similarity 92.0%; Pred. No. 5.1e-38;

Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNQKNYLAHYQKPGQSPKLLIYMASTR 60

150 DIELTQSPSSLAVSAGEEVTMTCKSSQSVLYSSNQKNYLAHYQKPGQSPKLLIYMASTR 209

QY 61 ESGVPDRFSGSGGTDTFTLTITSSVQAEDLAVYYCHQYLLSSYTFGGGTKLEIK 112

210 ESGVPDRFSGSGGTDTFTLTITSSVQAEDLAVYYCHQYLLSSYTFGGGTKLEIK 261

Db

RESULT 9

AAW90228

ID AAW90228 standard; protein; 268 AA.

XX

AC AAW90228;

XX

DT 10-MAY-1999 (first entry)

XX

DE Anti-B7.1/anti-B7.2 bispecific triabody II.

XX

KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;

KW T cell activation; inhibitor; graft versus host disease;

KW transplant rejection; allograft rejection; autoimmune disease; allergy;

KW therapy; human; triabody; antibody; B7-24; 1G10.

XX

OS Mus sp.

OS Synthetic.

OS Chimeric.

OS

XX

FH Key

FT Peptide

FT 1..39

FT /note= "g3p signal peptide"

FT 40..155

FT /note= "anti B7.1 Mab VH region"

FT 156..268

FT /note= "anti B7.2 Mab VL region"

FT Peptide

XX

XX WO9858965-A2.

XX

PD 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-EP003791.
PF
XX
PR 20-JUN-1997; 97EP-00870092.
XX
XX (INNO-) INNOGENETICS NV.
PA
XX
XX
PI Lorre K, Sablon E, Buyse M, Bosman A;
XX
XX WPI; 1999-105615/09.
DR N-PSDB; AAX01662.
XX
XX
PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection.
XX
XX
PS Example 7.3; Fig 38; 182pp; English.
XX
XX This polypeptide comprises a bispecific triabody composed of the VH
CC region of anti-B7.1 monoclonal antibody (Mab) B7-24 joined to the VL
CC region of anti-B7.2 Mab 1G10. A triabody is a mono- a bi- or a
CC trispecific molecule recognising simultaneously e.g. two B7.2 and one
CC B7.1 molecules. It has a rigid structure that prevents simultaneous
CC binding to the 3 targets. Each antigen-binding site is formed by pairing
CC of one VH and one VL domain from the same or from two different
CC polypeptides. The invention relates to novel molecules, including
CC triabodies, which can cross-link and/or cross-react with the
CC costimulatory molecules B7.1 and B7.2 expressed on professional antigen-
CC presenting cells, leading to the inhibition of antigen-specific T cell
CC activation. Methods are provided for the production of such B7-binding
CC molecules, and for their use in the treatment or prevention of diseases
CC of the immune system, in particular graft rejection, graft versus host
CC disease, allergy and autoimmune diseases (claimed)
XX
XX Sequence 268 AA:
SQ
Query Match 92.6%; Score 540; DB 2; Length 268;
Best Local Similarity 92.0%; Pred. No. 5.1e-38;
Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYMASTR 60
Db 156 DIELTQSPSSLAVSAGEEVTMTCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYMASTR 215
QY 61 ESGVDPDRFSGSGGTDFLTITSSVQAEIDLAVYVYCHOYLSSYTFGGGTKEIK 112
Db 216 ESGVDPDRFTGSGSGTDFSLTITSSVQAEIDLAVYVYCHOYLSSWTFGGGTKEIK 267
RESULT 10
AAW90224
ID AAW90224 standard; protein; 273 AA.
XX
AC AAW90224;
XX
DT 10-MAY-1999 (first entry)
XX
DE Anti-B7.1/anti-B7.2 bispecific diabody II.
XX
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
KW T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease; allergy;
KW therapy; human; diabody; antibody; B7-24; 1G10.
XX
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..39
FT Misc-difference 21 /note= "g3p signal peptide"
FT /note= "encoded by TCA"

FT Region 40..155
FT /note= "anti B7.1 Mab VH region"
FT Peptide 156..160
FT /note= "G4S flexible linker"
FT Region 161..273
FT /note= "anti B7.2 Mab VL region"
XX
XX WO9858965-A2.
XX
XX 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-EP003791.
XX
XX 20-JUN-1997; 97EP-00870092.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Lorre K, Sablon E, Buyse M, Bosman A;
XX
XX WPI; 1999-105615/09.
DR N-PSDB; AAX01658.
XX
XX
PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection.
XX
XX
PS Example 7.2; Fig 30; 182pp; English.
XX
XX This polypeptide comprises a bispecific diabody composed of the VH region
CC of anti-B7.1 monoclonal antibody (Mab) B7-24 joined via a short, flexible
CC linker to the VL region of anti-B7.2 Mab 1G10. Mono- or bispecific
CC bivalent molecules are generated by shortening the flexible linker
CC sequence between the VH and VL of the anti-B7.1 scFv B7-24, the anti-B7.2
CC scFv 1G10 and the scFv molecule with dual specificity for B7.1 and B7.2
CC (B7.12) to 5-10 residues, and for bispecific molecules by cross-pairing
CC the VH and VL domains from the 2 scFvs with different antigen recognition
CC (B7.1/B7.2 and B7.12/B7.12). The invention relates to novel molecules,
CC including diabodies, which can cross-link and/or cross-react with the
CC costimulatory molecules B7.1 and B7.2 expressed on professional antigen-
CC presenting cells, leading to the inhibition of antigen-specific T cell
CC activation. Methods are provided for the production of such B7-binding
CC molecules, and for their use in the treatment or prevention of diseases
CC of the immune system, in particular graft rejection, graft versus host
CC disease, allergy and autoimmune diseases (claimed)
XX
XX Sequence 273 AA:
SQ
Query Match 92.6%; Score 540; DB 2; Length 273;
Best Local Similarity 92.0%; Pred. No. 5.2e-38;
Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYMASTR 60
Db 161 DIELTQSPSSLAVSAGEEVTMTCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYMASTR 220
QY 61 ESGVDPDRFSGSGGTDFLTITSSVQAEIDLAVYVYCHOYLSSYTFGGGTKEIK 112
Db 221 ESGVDPDRFTGSGSGTDFSLTITSSVQAEIDLAVYVYCHOYLSSWTFGGGTKEIK 272
RESULT 11
AAW90218
ID AAW90218 standard; protein; 556 AA.
XX
AC AAW90218;
XX
DT 10-MAY-1999 (first entry)
XX
XX Bispecific tetravalent antibody BiTab1G10-B7-24H6.
XX
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
KW T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease; allergy;
KW therapy; human; bispecific tetravalent antibody; BiTab;

XX	WTAB1G10-B7-24H6.
OS	Mus sp.
OS	Homo sapiens.
OS	Synthetic.
OS	Chimeric.
XX	
FH	Key
FT	Region
FT	Peptide
FT	Region
FT	Region
FT	Domain
FT	Domain
FT	Region
FT	Peptide
FT	Region
FT	Peptide
PN	WO9858965-A2.
PD	30-DEC-1998.
PX	22-JUN-1998;
PR	20-JUN-1997;
PA	(INNO-) INNOGENETICS NV.
PI	Lorre K, Sablon E, Buysse M, Bosman A;
DR	WPI; 1999-105615/09.
DR	N-PSTDB; AAX01652.
XX	New molecules which bind B7.1 and B7.2 - useful to prevent and treat immune diseases including allograft rejection.
PS	Example 7.1; Fig 18; 182pp; English.
CC	This polypeptide comprises the bispecific tetraivalent antibody BiTab1G10-B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2 anti B7.2 scFvs (tetra valency). One single BiTab1 is a homodimer of 2 identical molecules, each containing both an anti B7.1 and anti B7.2 scFv (bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a dimerisation domain (see AA00219), which drives the homodimerisation of the molecule. DNA (see AAX01652) encoding the BiTab has been constructed to allow expression of the BiTab in transformed E. coli cells. The BiTab cross-links, and/or cross-reacts, with the costimulatory molecules B7.1 and B7.2 that are expressed on the membrane of professional antigen-presenting cells, leading to the inhibition of antigen-specific T cell activation. The invention relates to such B7-binding molecules, methods for their production, and their use for treating or preventing diseases of the immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed)
SO	Sequence 556 AA:
Query Match	92.6%; Score 540; DB 2; Length 556;
Best Local Similarity	92.0%; Pred. No. 1e-37;
Matches 103; Conservative	4; Mismatches 5; Indels 0; Gaps 0;

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Db      136 DIELTQSPSSILAVSAGEEVTMTCKSSQSVLYSSNQKNYLAAYQCKPGQSPKLLIYWASTR 193
QY      61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSSYTFGGGTKLEIK 112
        |||||...|||:|||||:|||||:|||||
Db      196 ESGVPDRFSGSGSGTDFSLTITSSVQAEDLAVYYCHQYLSSWTFGGGTKLEIK 247

RESULT 12
AAW90217
ID      AAW90217 standard; protein; 580 AA.
AC      XX
XX      AAW90217;
DT      10-MAY-1999 (first entry)
DE      Bispecific tetravalent antibody B1TAB7-24-IG10H6.
KW      B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
KW      T cell activation; inhibitor; graft versus host disease;
KW      transplant rejection; allograft rejection; autoimmune disease; allergy;
KW      therapy; human; bispecific tetravalent antibody; B1Tab;
KW      B1TAB7-24-IG10H6.
XX      Mus sp.
OS      Homo sapiens.
OS      Synthetic.
OS      Chimeric.
FH      Key
FT      Peptide
        Location/Qualifiers
        1..24
        /note= "pelB signal peptide"
FT      Region
        25..138
        /note= "VH region anti B7.1 MAb"
FT      Peptide
        139..153
        /note= "(G4S3) flexible linker"
FT      Region
        154..262
        /note= "VL region anti B7.1 MAb"
FT      Misc-difference
        261
        /note= "encoded by CTG"
FT      Region
        263..273
        /note= "human IgG3 hinge region"
FT      Domain
        274..308
        /note= "helix-turn-helix dimerisation domain"
FT      Domain
        309..319
        /note= "human IgG3 hinge domain"
FT      Region
        320..446
        /note= "VH region anti B7.2 MAb"
FT      Misc-difference
        322..327
        /note= "codons for these amino acids are not present in
the DNA sequence for B1TAB7-24-IG1-H6 provided in the
specification"
FT      Peptide
        447..461
        /note= "(G4S3)flexible linker"
FT      Region
        462..574
        /note= "VL region anti B7.2 MAb"
FT      Peptide
        575..580
        /note= "His6 tag"
PN      WO9858965-A2.
XX
PD      30-DEC-1998.
XX
XX      22-JUN-1998; 98WO-EP003791.
PF
XX      20-JUN-1997; 97EP-00870092.
PR
PA      (INNO-) INNOGENETICS NV.
XX
XX      Lorre K, Sablon E, Buyse M, Bosman A;
PI      WPI; 1999-105615/09.
DR      N-PSDB; AAX01651.
XX

```


PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection.
XX
PS Example 7.1; Fig 16; 182pp; English.
XX
CC This polypeptide comprises the bispecific tetravalent antibody BiTabB7-24
CC -1G10H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2
CC anti B7.2 scFvs (tetravalency). One single BiTab is a homodimer of 2
CC identical molecules, each containing both an anti B7.1 and anti B7.2 scFv
CC (bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a
CC dimerisation domain (see AAW90219), which drives the homodimerisation of
CC the molecule. DNA (see AAX01651) encoding the BiTab has been constructed
CC to allow expression of the BiTab in transformed E. coli cells. The BiTab
CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1
CC and B7.2 that are expressed on the membrane of professional antigen-
CC presenting cells, leading to the inhibition of antigen-specific T cell
CC activation. The invention relates to such B7-binding molecules, methods
CC for their production, and their use for treating or preventing diseases
CC of the immune system, in particular graft rejection, graft versus host
CC disease, allergy and autoimmune diseases (claimed)
XX
SQ Sequence 580 AA;

Query Match 92.6%; Score 540; DB 2; Length 580;
Best Local Similarity 92.0%; Pred. No. 1.1e-37;
Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERVTWNCSSQSVLYSSNQKNYLAWYQKPGQSPKLLIYMASTR 60
Db 462 DIELTQSPSSLAVSAGEEVTMTCKSSQSVLYSSNQKNYLAWYQKPGQSPKLLIYMASTR 521

QY 61 ESGVPPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLTSSYTFGGGTKEIK 112
Db 522 ESGVPPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLTSSYTFGGGTKEIK 573

RESULT 13
ABG31024
ID ABG31024 standard; protein; 272 AA.
XX
AC ABG31024;
XX
DT 05-NOV-2002 (first entry)
XX
DE Synthetic mouse fusion protein.
XX
KW Immunosuppressive; antirheumatic; antithyroid; antidiabetic; mouse;
KW neuroprotective; gene therapy; single chain antibody; variable fragment;
KW scFv; binding domain-immunoglobulin fusion protein; B-cell disorder;
KW malignant condition; rheumatoid arthritis; myasthenia gravis; psoriasis;
KW Grave's disease; Hashimoto's thyroiditis; type I diabetes mellitus;
KW multiple sclerosis; systemic lupus erythematosus; Sjogrens syndrome;
KW immune thrombocytopenic purpura; scleroderma; cancer; Chron's disease;
KW ulcerative colitis; inflammatory bowel disease; immunological effector;
KW cell mediated cytotoxicity; complement dependent cytotoxicity;
KW complement fixation; mouse.
XX
XX Mus musculus.
OS Synthetic.
OS
XX WO200256910-A1.
PN
XX 25-JUL-2002.
PD
XX 17-JAN-2002; 2002WO-US001487.
PF
XX 17-JAN-2001; 2001US-00765208.
PR
XX (GENE-) GENECRAFT INC.
PA
XX Ledbetter JA, Hayden-Ledbetter M;
PI
XX WPI; 2002-599691/64.
DR

DR N-PSDB; ABK89856.
XX
PT New human binding domain-immunoglobulin fusion protein useful for
PT treating a subject having or suspected of having a B-cell disorder or
PT malignant condition e.g. rheumatoid arthritis.
XX
PS Disclosure; Page 119; 136pp; English.
XX
CC The invention describes a binding domain-immunoglobulin fusion protein
CC that is capable of at least one immunological activity, comprising a
CC binding domain polypeptide fused to an immunoglobulin hinge region
CC polypeptide capable of specifically binding to an antigen, or an
CC immunoglobulin heavy chain CH2 or CH3 constant region polypeptide fused
CC to the hinge region polypeptide or to the CH2 constant region
CC polypeptide. The fusion protein is useful for treating a subject having
CC or suspected of having a B-cell disorder or malignant condition e.g.
CC rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's
CC thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus
CC erythematosus, Sjogrens syndrome, immune thrombocytopenic purpura,
CC psoriasis, scleroderma, cancer and inflammatory bowel disease such as
CC Chron's disease and ulcerative colitis. The fusion protein retains the
CC ability to participate in well known immunological effector activities
CC including antibody dependent cell mediated cytotoxicity and/or complement
CC fixation in complement dependent cytotoxicity, despite having structures
CC that would not be expected to be capable of promoting the effector
CC activities. It can be produced in substantial quantities that are
CC typically greater than those routinely attained with single-chain
CC antibody constructs. This is the amino acid sequence of a synthetic mouse
CC immunoglobulin fusion protein
XX
SQ Sequence 272 AA;

Query Match 91.4%; Score 533; DB 5; Length 272;
Best Local Similarity 89.3%; Pred. No. 2e-37;
Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERVTWNCSSQSVLYSSNQKNYLAWYQKPGQSPKLLIYMASTR 60
Db 21 NIMMTQSPSSLAVSAGEKVTWNCSSQSVFYSSNQKNYLAWYQKPGQSPKLLIYMASTR 80

QY 61 ESGVPPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLTSSYTFGGGTKEIK 112
Db 81 ESGVPPDRFSGSGSGTDFTLTITSSVHTEDLAVYYCHQYLTSSYTFGGGTKEIK 132

RESULT 14
ADD25453
ID ADD25453 standard; protein; 272 AA.
XX
AC ADD25453;
XX
DT 15-JAN-2004 (first entry)
XX
DE Binding domain-immunoglobulin fusion protein-associated protein #4.
XX
KW Binding domain; immunoglobulin; fusion protein; cyostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
XX Unidentified.
OS
XX US2003118592-A1.
PN
XX 26-JUN-2003.
PD
XX 25-JUL-2002; 2002US-00207655.
PF
XX 17-JAN-2001; 2001US-0367358P.
PR

PR 17-JAN-2002; 2002US-00053530.
PR 03-JUN-2002; 2002US-0385691P.
XX
XX
PA (GENE-) GENE-CRAFT INC.
XX
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
XX WPI; 2003-801317/75.
DR

PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
XX

PS Disclosure; SEQ ID NO 14; 157bp; English.

XX
CC The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide;
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX
XX

SQ Sequence 272 AA;

Query Match 91.4%; Score 533; DB 7; Length 272;
Best Local Similarity 89.3%; Pred. No. 2e-37;
Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
21 NIMTQSPSSSLAVSAGEKVTMCKSSQSVFYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 80
QY 61 ESGVDPDRFSGSGSGTDFTLTSSVQAEDLAVYYCHQYLSSYTFGGGTKEIK 112
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
81 ESGVDPDRFSGSGSGTDFTLTSSVQAEDLAVYYCHQYLSSYTFGGGTKEIK 132

RESULT 15
AAR92215

ID AAR92215 standard; protein; 113 AA.
XX
XX AAR92215;
AC
XX
XX 28-MAY-1996 (first entry)
DT
XX
XX LL2 MAb VK region.
DE
XX
XX Humanised antibody; monoclonal antibody; MAb; LL2; B-cell lymphoma;
KW leukaemia; therapy; diagnosis; complementarity determining region; CDR;
KW antibody engineering.
XX
XX Mus musculus.
OS

XX
FH Key Location/Qualifiers
FT Region 24..40
FT /label= CDR1
FT /note= "claim 6, page 44"
FT Region 56..62
FT /label= CDR2
FT /note= "claim 7, page 44"
FT Region 95..103
FT /label= CDR3
FT /note= "claim 8, page 44"

PN WO9604925-A1.
XX
XX 22-FEB-1996.
XX
XX 11-AUG-1995; 95WO-US009641.
XX
XX 12-AUG-1994; 94US-00289576.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX

PI Leung S, Hansen H;
XX
XX WPI; 1996-139454/14.
DR N-PSDB; AAT15802.
DR

XX
PT Chimeric and humanised LL2 antibodies - used to produce conjugates for
PT the therapy and diagnosis of B-cell lymphoma(s) and leukaemia(s).
XX
XX Claim 5; Page 35-36; 70pp; English.

CC The complementarity determining regions (CDRs) of mouse monoclonal
CC antibody (MAb) LL2 VK (AAR92215) and VH (AAR92216) regions were
CC recombinantly linked to the framework sequences of human VK and VH
CC regions, respectively, to give humanised LL2 VK (AAR92217) and VH
CC (AAR92218). These were subsequently linked, respectively, to human kappa
CC and IgG1 constant regions. A humanised MAb was obtained that retained the B-
CC lymphoma and leukaemia cell targeting and internalisation characteristics
CC of the parental LL2 MAb, and which exhibited a lowered HAMA reaction. It
CC can be linked to e.g. a cytostatic agent for therapeutic appln
XX
XX

SQ Sequence 113 AA;

Query Match 90.4%; Score 527; DB 2; Length 113;
Best Local Similarity 88.4%; Pred. No. 2.8e-37;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 DIQLTQSPSSSLAVSAGENVTMCKSSQSVLYSANHKNYLAWYQOKPGQSPKLLIYMASTR 60
QY 61 ESGVDPDRFSGSGSGTDFTLTSSVQAEDLAVYYCHQYLSSYTFGGGTKEIK 112
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 ESGVDPDRFSGSGSGTDFTLTSSVQAEDLAVYYCHQYLSSYTFGGGTKEIK 112

Search completed: March 26, 2004, 05:03:59
Job time : 46.4965 secs

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CM protein - protein search, using sw model

Run on: March 26, 2004, 05:00:12 ; Search time 11.7163 Seconds
(without alignments)
493.509 Million cell updates/sec

Title: US-10-056-052A-18
Perfect score: 583
Sequence: 1 DIVMTQSPDSLAVSLGERVT.....YCHOYLSSYTFGGTKLEIK 112

Scoring table: BLCSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ISSUED_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	94.5	112	4	US-08-435-516-28 Sequence 28, Appl
2	527	90.4	113	1	US-08-690-102A-2 Sequence 2, Appli
3	527	90.4	113	3	US-09-127-902-2 Sequence 2, Appli
4	527	90.4	113	3	US-09-155-107-2 Sequence 2, Appli
5	527	90.4	113	5	PCT-US95-09641-2 Sequence 2, Appli
6	525.5	90.1	113	5	PCT-US93-08435-6 Sequence 6, Appli
7	521	89.4	112	1	US-07-942-245-30 Sequence 30, Appl
8	521	89.4	112	2	US-07-916-098A-15 Sequence 15, Appl
9	520.5	89.3	113	4	US-09-274-163E-16 Sequence 16, Appl
10	520.5	89.3	113	5	PCT-US93-08435-8 Sequence 8, Appli
11	520.5	89.3	155	3	US-08-828-741B-11 Sequence 11, Appl
12	520.5	89.3	155	4	US-09-160-567-11 Sequence 11, Appl
13	520.5	89.3	155	4	US-09-160-567-11 Sequence 11, Appl
14	520.5	89.3	155	4	US-09-509-031-11 Sequence 11, Appl
15	520.5	89.3	342	3	US-08-828-741B-6 Sequence 6, Appli
16	520.5	89.3	342	4	US-09-160-567-6 Sequence 6, Appli
17	520.5	89.3	342	4	US-09-710-299-6 Sequence 6, Appli
18	520.5	89.3	342	4	US-09-509-031-6 Sequence 6, Appli
19	520.5	89.3	495	3	US-08-828-741B-4 Sequence 4, Appli
20	520.5	89.3	495	4	US-09-160-567-4 Sequence 4, Appli
21	520.5	89.3	495	4	US-09-509-031-4 Sequence 4, Appli
22	520.5	89.3	495	4	US-09-509-031-4 Sequence 4, Appli
23	516.5	88.6	113	4	US-08-961-309-73 Sequence 73, Appl
24	516.5	88.6	114	4	US-09-274-163E-2 Sequence 2, Appli
25	516.5	88.6	114	4	US-09-274-163E-6 Sequence 6, Appli
26	515.5	88.4	114	4	US-09-274-163E-4 Sequence 4, Appli
27	515	88.3	241	2	US-07-916-098A-56 Sequence 56, Appl

28	513.5	88.1	113	4	US-08-525-539A-80	Sequence 80, Appl
29	512.5	87.9	133	3	US-08-463-903-4	Sequence 4, Appli
30	512.5	87.9	133	4	US-07-935-695-4	Sequence 4, Appli
31	512.5	87.9	134	4	US-08-961-309-58	Sequence 58, Appl
32	512.5	87.9	274	4	US-08-961-309-66	Sequence 66, Appl
33	512.5	87.9	275	3	US-08-463-903-6	Sequence 6, Appli
34	512.5	87.9	275	4	US-07-935-695-6	Sequence 6, Appli
35	511.5	87.7	114	4	US-09-025-769B-17	Sequence 17, Appl
36	510.5	87.6	113	3	US-08-483-749A-16	Sequence 16, Appl
37	510.5	87.6	171	3	US-08-463-903-20	Sequence 20, Appl
38	510.5	87.6	171	4	US-07-935-695-20	Sequence 20, Appl
39	510	87.5	141	4	US-09-582-337-16	Sequence 16, Appl
40	507.5	87.0	114	1	US-08-360-125-6	Sequence 6, Appli
41	507.5	87.0	114	2	US-08-450-578-6	Sequence 6, Appli
42	507.5	87.0	114	2	US-09-017-628-6	Sequence 6, Appli
43	507.5	87.0	114	2	US-09-014-880-6	Sequence 6, Appli
44	507.5	87.0	114	4	US-08-450-363-6	Sequence 6, Appli
45	506.5	86.9	260	3	US-08-463-903-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-435-516-28
; Sequence 28, Application US/08435516
; Patent No. 6500931
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
; FILING DATE: 04-NOV-1992; -02-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-435-516-28

Query Match 94.5%; Score 551; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.4e-44;
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY	1	DIVMTQSPDSLAVSLGERVTNCKSSQSVLYSSNQKYLAWYQOKPGQSPKLLIYMASTR 60
DB	1	NIVMTQSPDSLAVSAGEKVTNCKSSQSVLYSSNQKYLAWYQOKPGQSPKLLIYMASTR 60
QY	61	ESGVPRFSSGSGTDFLTLSVQAEPLAVYCHQYLSSYTFGGTKLEIK 112
DB	61	ESGVPRFSSGSGTDFLTLSVQAEPLAVYCHQYLSSYTFGGTKLEIK 112


```
RESULT 2
US-08-690-102A-2
; Sequence 2, Application US/08690102A
; Patent No. 5789554
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,102A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-690-102A-2

Query Match      90.4%; Score 527; DB 1; Length 113;
Best Local Similarity 88.4%; Pred. No. 2.5e-42;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLAIVSAGENVTMCKSSQSVLYSANHKNYLAWYQOKPGQSPKLLIYMASTR 60

QY 61 ESGVDPDRFSGSGGTDTFTLTISSVQAEDLAVYCHQYLSSYTFGGGTGLEIK 112
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ESGVDPDRFSGSGGTDTFTLTISRQVEDLAIYCHQYLLSSWTFGGGTGLEIK 112

RESULT 3
US-09-127-902-2
; Sequence 2, Application US/09127902
; Patent No. 6187287
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
```

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ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,902
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,102
; FILING DATE: 01-JUL-1996
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-127-902-2
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Query Match      90.4%; Score 527; DB 3; Length 113;
Best Local Similarity 88.4%; Pred. No. 2.5e-42;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPSSLAIVSAGENVTMCKSSQSVLYSANHKNYLAWYQOKPGQSPKLLIYMASTR 60

QY 61 ESGVDPDRFSGSGGTDTFTLTISSVQAEDLAVYCHQYLSSYTFGGGTGLEIK 112
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ESGVDPDRFSGSGGTDTFTLTISRQVEDLAIYCHQYLLSSWTFGGGTGLEIK 112
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```
RESULT 4
US-09-155-107-2
; Sequence 2, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; EARLIER FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
;
US-09-155-107-2
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Query Match      90.4%; Score 527; DB 3; Length 113;
Best Local Similarity 88.4%; Pred. No. 2.5e-42;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
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Db 1 DIQLTQSPSLAVSAGENVMTWCKSSQSVLYSANHKNYLAWYQOKPGQSPKLLIYMASTR 60
QY 61 ESGVDPDRFSGSGSGTDFLTITSSVQAEDLAVYYCHQYLSSTFGGKTLEIK 112
Db 61 ESGVDPDRFSGSGSGTDFLTITSSVQAEDLAVYYCHQYLSSTFGGKTLEIK 112

RESULT 5

PCT-US95-09641-2
; Sequence 2, Application PC/TUS9509641
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09641
; FILING DATE: 11-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09641-2

Query Match 90.4%; Score 527; DB 5; Length 113;
Best Local Similarity 88.4%; Pred. No. 2.5e-42;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERVTNCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
Db 1 DIQLTQSPSLAVSAGENVMTWCKSSQSVLYSANHKNYLAWYQOKPGQSPKLLIYMASTR 60
QY 61 ESGVDPDRFSGSGSGTDFLTITSSVQAEDLAVYYCHQYLSSTFGGKTLEIK 112
Db 61 ESGVDPDRFSGSGSGTDFLTITSSVQAEDLAVYYCHQYLSSTFGGKTLEIK 112

RESULT 6

PCT-US93-08435-6
; Sequence 6, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Confering Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SBC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-08435-6

Query Match 90.1%; Score 525.5; DB 5; Length 113;
Best Local Similarity 90.3%; Pred. No. 3.5e-42;
Matches 102; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTNCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
Db 1 DIQLTQSPDSLAVSLGERVTNCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYMASTR 60
QY 61 ESGVDPDRFSGSGSGTDFLTITSSVQAEDLAVYYCHQYLSSTFGGKTLEIK 112
Db 61 ESGVDPDRFSGSGSGTDFLTITSSVQAEDLAVYYCHQYLSSTFGGKTLEIK 112

RESULT 7

US-07-942-245-30
; Sequence 30, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrie, Mion, Zimm, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-07-942-245-30

Query Match	89.4%;	Score 521;	DB 1;	Length 112;
Best Local Similarity	89.3%;	Pred. No. 9e-42;		
Matches 100;	Conservative	5;	Mismatches 7;	Indels 0;
				Gaps 0;

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QY      1 DIVMTQSPDLSLGLGERVTMCKSSQSQSVLYSSNQNYLAWYQQKPGQSPKLLIYWASTR 60
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DB      1 DIVMTQSPDSLAVSLGERATINCKSSQSQSVLYSSNNKNYLAWYQQKPGQP KLLIYWASTR 60
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QY      61 ESGVPDRFSGSGSCTDFTLTITSSVQAEADLAVYYCHQYLISSYTFGGGSKLEIK 112
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 ESGVPDRFSGSGSCTDFTLTITSSVQAEADLAVYYCQYLTPTFGGGKVEIK 112
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RESULT 8
US-07-916-098A-15
; Sequence 15, Application US/07916098A
; Patent No. 5871732

```

: GENERAL INFORMATION:
: APPLICANT: BURKLY, LINDA C.
: APPLICANT: CHISHOLM, PATRICIA L.
: APPLICANT: THOMAS, DAVID W.
: APPLICANT: ROSA, MARGARET D.
: APPLICANT: ROSA, JOSEPH J.
: TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
: TITLE OF INVENTION: PROCHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
: NUMBER OF SEQUENCES: 61
: CORRESPONDENCE ADDRESS:
:

```

```

: ADDRESSSEE: ALLEGRETTI & WITCOFF, LTD.
: STREET: 10 SOUTH WACKER DRIVE
: CITY: CHICAGO
: STATE: ILLINOIS
: COUNTRY: U.S.A.
: ZIP: 60606
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORD PERFECT 5.1
: CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/07/916,098A
 ; FILING DATE: July 24, 1992
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/08843
 ; FILING DATE: No. 5871732ember 27, 1991
 ; CLASSIFICATION: 424
 ; APPLICATION NUMBER: 07/618,542
 ; FILING DATE: No. 5871732ember 27, 1990

```

: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: JOHN J. MC DONNELL
: REGISTRATION NUMBER: 26,944
: REFERENCE/DOCKET NUMBER: 9
: TELECOMMUNICATION INFORMATION
: TELEPHONE: (312) 715-1000
: TELEFAX: (312) 715-1234
: TELEX: 910/221-5317
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 112 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-07-916-098A-15

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Query Match	89.4%;	Score 521;	DB 2;	Length 112;
Best Local Similarity	89.3%;	Pred. No. 9e-42;		
Matches 100; Conservative	6;	Mismatches	6;	Indels 0;
				Gaps 0;

QY 1 DIVMTQSPDLSAVSLGERVTMNCSSQSVLYSSNQKNTLAMYQOKPGQSPKLLIYVASTR 60

Db 1 DIVMTQSPSSLAVSGEKTMI CKSSQSLYSTNQKNYLAWYQQKPGQSPKLLIYWA STR 60

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QY      61  ESGYDRFSGSGSGTDFLTLLISSVQAEADLAVYYCHQYLLSYTFGGGTKEIK 112
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DB      61  ESGYDRFTGSGSGTDFLTLLISSVKAEDLAVYYCQYYSYRTFGGTKEIK 112
      |||||:|||||:|||||

```

RESULT 9
US-09-274-163E-16
; Sequence 16, Application US/09274163E

```

; Patent No. 6485943
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: WILKINS STEVENS, Priscilla
; APPLICANT: RAFFEN, Rosemarie
; APPLICANT: SCHIFFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 051583/0224
; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 08/373,380
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-274-163E-16

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Query Match	89.3%	Score 520.5;	DB 4;	Length 113;
Best Local Similarity	89.4%;	Pred. No. 1e-41;		
Matches 101; Conservative	5;	Mismatches	6;	Indels 1; Gaps 1;

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QY      1 DIVMTSPDSLAVSLGERVTMNCCKSSQSVLYSSNQKNYLAWYQQKPQSFKLLIYNASTR    600
        ||||| : |||||
DB      1 DIVMTSPDSLAVSLGERATINCKSSQSVLYSSNKNYLAWYQQKPGQPCKLLIYNASTR    600
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QY      61  EGVPPDRFSGSGGSTDFTLTITSSVQAEADLAVYCHQYLSS-YTFGGGTKEIK 112
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      61  EGVPPDRFSGSGGSTDFTLTITSSVQAEADLAVYCHQYLSS-YTFGGGTKEIK 113

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RESULT 10
PCT-US93-08435-8
; Sequence 8, Application PC/TUS9308435

GENERAL INFORMATION:
APPLICANT: Smithkline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:

ADDRESSSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE: :
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654


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RESULT 13
US-09-710-299-11
; Sequence 11, Application US/09710299
; Patent No. 6521741
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
;           Suess, Gabriele M.
;           Tarlinton, David M.
;           Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
;                   PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/710,299
; FILING DATE: 09-No. 6521741-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,741
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-710-299-11

Query Match      89.3%; Score 520.5; DB 4; Length 155;
Best Local Similarity 89.4%; Pred. No. 1.4e-41;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

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Db      30 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWYQOKPGQSPKLLIYWASTR 89

QY      61 ESGVPRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSS-YTFGGGTKLEIK 112
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RESULT 14
US-09-509-031-11
; Sequence 11, Application US/09509031
; Patent No. 6590080
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
;           Suess, Gabriele M.
;           Tarlinton, David M.
;           Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/09/509,031

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; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Kappa
US-09-509-031-11

Query Match      89.3%; Score 520.5; DB 4; Length 155;
Best Local Similarity 89.4%; Pred. No. 1.4e-41;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY      1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNQKNTLAWYQOKPGQSPKLLIYWASTR 60
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QY      61 ESGVPRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSS-YTFGGGTKLEIK 112
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Db      90 ESGVPRFSGSGSGTDFTLTITSSVQAEDVAVYYCQQYSTPYSFGGTGLEIK 142

RESULT 15
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; Sequence 6, Application US/08828741B
; Patent No. 6043069
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
;           Suess, Gabriele M.
;           Tarlinton, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
;                   PRODUCING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,741B
; FILING DATE: 26-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10591
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-828-741B-6

Query Match      89.3%; Score 520.5; DB 3; Length 342;
Best Local Similarity 89.4%; Pred. No. 3.4e-41;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

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Qy	61	ESGVFDRFSSGSGTDFTLTSSVQAE DLAVYCHQYLSS-YTFGGTKLEIK	112
Db	90	ESGVFDRFSSGSGTDFTLTSSVQAE DLAVYCHQYLSS-YTFGGTKLEIK	142

Search completed: March 26, 2004, 05:11:18
Job time : 41.7163 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2004, 05:07:57 ; Search time 353.277 Seconds
(without alignments)
82.955 Million cell updates/sec

Title: US-10-056-052a-18
Perfect score: 583
Sequence: 1 DIVMTQSPDSLAVSLGERVT.....YCHQYLSSYTFGGGTKLEIK 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCR_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/PCRUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	583	100.0	112	14	US-10-056-052-18 Sequence 18, Appl
2	553	94.9	112	14	US-10-056-052-10 Sequence 10, Appl
3	551	94.5	112	14	US-10-229-335-28 Sequence 28, Appl
4	545	93.5	112	14	US-10-056-052-6 Sequence 6, Appl
5	544	93.3	112	14	US-10-056-052-14 Sequence 14, Appl
6	533	91.4	272	14	US-10-207-655-14 Sequence 14, Appl
7	533	91.4	272	14	US-10-053-530-14 Sequence 14, Appl
8	527	90.4	113	9	US-09-741-843-2 Sequence 2, Appl
9	527	90.4	113	10	US-09-894-839-2 Sequence 2, Appl
10	527	90.4	113	10	US-09-988-013A-2 Sequence 2, Appl
11	527	90.4	113	15	US-10-446-689-2 Sequence 2, Appl
12	520.5	89.3	113	9	US-09-274-163E-16 Sequence 16, Appl
13	520.5	89.3	155	14	US-10-345-618-11 Sequence 11, Appl
14	520.5	89.3	342	14	US-10-345-618-6 Sequence 6, Appl
15	520.5	89.3	495	14	US-10-345-618-4 Sequence 4, Appl

16	516.5	88.6	113	14	US-10-255-478-73	Sequence 73, Appl
17	516.5	88.6	114	9	US-09-274-163E-2	Sequence 2, Appl
18	516.5	88.6	114	9	US-09-274-163E-6	Sequence 6, Appl
19	516	88.5	130	13	US-10-146-305-7	Sequence 7, Appl
20	515.5	88.4	114	9	US-09-274-163E-4	Sequence 4, Appl
21	513.5	88.1	113	9	US-09-956-206A-80	Sequence 80, Appl
22	512.5	87.9	134	14	US-10-255-478-58	Sequence 58, Appl
23	512.5	87.9	240	9	US-09-799-514-8	Sequence 8, Appl
24	512.5	87.9	274	14	US-10-255-478-66	Sequence 66, Appl
25	510.5	87.6	113	10	US-09-995-529-6	Sequence 6, Appl
26	510.5	87.6	119	14	US-10-010-729-13	Sequence 13, Appl
27	510	87.5	141	14	US-10-390-986-16	Sequence 16, Appl
28	507.5	87.0	114	15	US-09-810-502-38	Sequence 38, Appl
29	507.5	87.0	264	15	US-10-264-049-4274	Sequence 4274, Ap
30	506.5	86.9	260	14	US-10-255-478-64	Sequence 64, Appl
31	506.5	86.9	284	14	US-10-255-478-70	Sequence 70, Appl
32	505.5	86.7	122	14	US-10-010-729-51	Sequence 51, Appl
33	503.5	86.4	113	14	US-10-121-464-6	Sequence 6, Appl
34	503.5	86.4	113	14	US-10-121-464-6	Sequence 34, Appl
35	503.5	86.4	113	14	US-10-159-006-34	Sequence 6, Appl
36	503.5	86.4	114	14	US-10-125-687-11	Sequence 11, Appl
37	502.5	86.2	135	14	US-10-171-452A-1	Sequence 1, Appl
38	502.5	86.2	135	15	US-10-353-708-1	Sequence 1, Appl
39	500	85.8	113	9	US-09-741-843-6	Sequence 6, Appl
40	500	85.8	113	10	US-09-894-839-6	Sequence 6, Appl
41	500	85.8	113	10	US-09-988-013A-6	Sequence 6, Appl
42	500	85.8	113	15	US-10-446-689-6	Sequence 6, Appl
43	499.5	85.7	113	14	US-10-121-464-2	Sequence 2, Appl
44	499.5	85.7	113	14	US-10-159-006-2	Sequence 2, Appl
45	499.5	85.7	113	14	US-10-159-006-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-10-056-052-18

/ Sequence 18, Application US/10056052

/ Publication No. US20030099656A1

/ GENERAL INFORMATION:

/ APPLICANT: PATTI, Joseph M

/ APPLICANT: HUTCHINS, Jeff T

/ APPLICANT: DOMANSKI, Paul

/ APPLICANT: PATEL, Pratiksha

/ APPLICANT: HALU, Andrea

/ TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .

/ FILE REFERENCE: P07069US04/BAS

/ CURRENT APPLICATION NUMBER: US/10/056,052

/ CURRENT FILING DATE: 2002-04-19

/ PRIOR APPLICATION NUMBER: 60/308,116

/ PRIOR FILING DATE: 2001-07-30

/ PRIOR APPLICATION NUMBER: 60/298,413

/ PRIOR FILING DATE: 2001-06-18

/ PRIOR APPLICATION NUMBER: 60/274,611

/ PRIOR FILING DATE: 2001-03-12

/ PRIOR APPLICATION NUMBER: 60/264,072

/ PRIOR FILING DATE: 2001-01-26

/ NUMBER OF SEQ ID NOS: 20

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 18

/ LENGTH: 112

/ TYPE: PRT

/ ORGANISM: Staphylococcus aureus

/ US-10-056-052-18

Query Match 100.0%; Score 583; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.3e-48;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNTLAWYQOKPGQSPKLLIYMASTR 60
DB 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNTLAWYQOKPGQSPKLLIYMASTR 60

QY 61 ESGVPDRFSGSGGTDFTLTITSSVQAEDLAVYYCHQYLSSTYFGGGTKLEIK 112
Db 61 ESGVPDRFSGSGGTDFTLTITSSVQAEDLAVYYCHQYLSSTYFGGGTKLEIK 112

RESULT 2

US-10-056-052-10
; Sequence 10, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-10

Query Match 94.9%; Score 553; DB 14; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.1e-45;
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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QY 61 ESGVPDRFSGSGGTDFTLTITSSVQAEDLAVYYCHQYLSSTYFGGGTKLEIK 112
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RESULT 3

US-10-229-335-28
; Sequence 28, Application US/10229335
; Publication No. US20030144483A1
; GENERAL INFORMATION:
; APPLICANT: MEDAREX, INC.
; TITLE OF INVENTION: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; STREET: P.O. Box 953, 1545 Route 22 East
; CITY: Annandale
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/229,335
; FILING DATE: 26-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516

; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-229-335-28

Query Match 94.5%; Score 551; DB 14; Length 112;
Best Local Similarity 93.8%; Pred. No. 4.8e-45;
Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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QY 61 ESGVPDRFSGSGGTDFTLTITSSVQAEDLAVYYCHQYLSSTYFGGGTKLEIK 112
Db 61 ESGVPDRFSGSGGTDFTLTITSSVQAEDLAVYYCHQYLSSTYFGGGTKLEIK 112

RESULT 4

US-10-056-052-6
; Sequence 6, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-6

Query Match 93.5%; Score 545; DB 14; Length 112;
Best Local Similarity 92.0%; Pred. No. 1.8e-44;
Matches 103; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

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Db 1 NIMMTQSPSSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAWYQKPGQSPKLLIYWASTR 60
QY 61 ESGVPDRFSGSGGTDFTLTITSSVQAEDLAVYYCHQYLSSTYFGGGTKLEIK 112
Db 61 ESGVPDRFSGSGGTDFTLTITSSVQAEDLAVYYCHQYLSSTYFGGGTKLEIK 112


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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Escherichia coli*
; US-09-274-163E-16

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Query Match	89.3%;	Score 520.5;	DB 9;	Length 113;
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Matches 101; Conservative	5;	Mismatches 6;	Indels 1;	Gaps 1;

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RESULT 13
US-10-345-618-11

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: Sequence 11, Application US/10345618
: Publication No. US20030148484A1
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: GENERAL INFORMATION:
: APPLICANT: Koentgen, Frank
: APPLICANT: Suess, Gabriele M.
: APPLICANT: Tarlington, David M.
: APPLICANT: Treutlein, Herbert R.
: TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
: FILE REFERENCE: 13474
: CURRENT APPLICATION NUMBER: US/10/345,618
: CURRENT FILING DATE: 2003-01-16
: PRIOR APPLICATION NUMBER: US/09/509,031
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 11
: LENGTH: 155
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: TYPE: PRT
: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: Description of Artificial Sequence:Kappa
:
: OTHER INFORMATION: protein sequence
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US-10-345-618-11

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Query Match 89.3%; Score 520.5; DB 14; Length 155;
Best Local Similarity 89.4%; Pred. NO. 5.5e-42;
Matches 101; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

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Oy      61 ESGVYDRFSGSGSSTDTLTITSSVQAEADLAVYYCHQYLSS-YTFGGGTKEIK 112
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Db      90 ESGVYDRFSGSGSSTDTLTITSSVQAEADLAVYYCQQYVSTPYSFQGQTKLEIK 142

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RESULT 14
US-10-345-618-6

; APPLICANT: Koentgen, Frank
 ; APPLICANT: Suess, Gabriele M.
 ; APPLICANT: Tarlington, David M.
 ; APPLICANT: Treutlein, Herbert R.
 ; TITLE OF INVENTION: CATALYTIC ANTIBOIDS AND A METHOD OF PRODUCING SAME
 ; FILE REFERENCE: 13474
 ; CURRENT APPLICATION NUMBER: US/10/345,618
 ; CURRENT FILING DATE: 2003-01-16
 ; PRIORITY APPLICATION NUMBER: US/09/509,031
 ;

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; PRIOR FILING DATE: 2000-06-09
;
; NUMBER OF SEQ ID NOS: 16
;
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 6

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; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:TIHL protein
; OTHER INFORMATION: sequence
US-10-345-618-6

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Query Match	89.3%;	Score 520.5;	DB 14;	Length 342;
Best Local Similarity	89.4%;	Pred. No. 1.3e-41;		
Matches 101;	Conservative	5;	Mismatches 6;	Indels 1;
				Gaps 1;

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QY      1 DIVMTQSPDLSAVSLGERVTMNCSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYASTR 60
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Db      30 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYASTR 89

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QY      61  ESGVPDRFSGSGGTDFTLTISVQAEDLAVYYCHQYLSS-YTFGGGTKEIK 112
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Db      90  ESGVPDRFSGSGGTDFTLTISLQAEDAVYYCQYSTPYSFGGQTKLEIK 142

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RESULT 15
US-10-345-618-4

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1 Sequence 4, Application US/10345618
2 Publication No. US20030148484A1
3 GENERAL INFORMATION:
4 APPLICANT: Koentgen, Frank
5 APPLICANT: Suess, Gabriele M.
6 APPLICANT: Tarlinton, David M.
7 APPLICANT: Treutlein, Herbert R.
8 TITLE OF INVENTION: CATALYTIC ANTIPOIDES AND A METHOD OF PRODUCING SAME
9 FILE REFERENCE: 13474
10 CURRENT APPLICATION NUMBER: US/10/345,618
11 CURRENT FILING DATE: 2003-01-16
12 PRIOR APPLICATION NUMBER: US/09/509,031
13 PRIOR FILING DATE: 2000-06-09
14 NUMBER OF SEQ ID NOS: 16
15 SOFTWARE: PatentIn Ver. 2.1
16 SEQ ID NO 4
17 LENGTH: 495
18 TYPE: PRT
19 ORGANISM: Artificial Sequence
20 FEATURE:
21 OTHER INFORMATION: Description of Artificial Sequence:CATAB-TEV
22 OTHER INFORMATION: protein sequence
23 US-10-345-618-4

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Query Match	89.3%;	Score 520.5;	DB 14;	Length 495;
Best Local Similarity	89.4%;	Pred. No. 2e-41;		
Matches 101; Conservative	5;	Mismatches	6;	Indels 1; Gaps 1;

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QY      1 DIWVTQS PDSLAVSLGERVTMNCSSQS SVLYSSNQKNIAWYQQKPGOSP KLLIYWASTR 60
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     30 DIWVTQS PDSLAVSLGERATINCKSSQS SVLYSSNSKNIAWYQQKPGOP KLLIYWASTR 89
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QY      61  ESGVEDRFSGSGSSTDFTLTSSVQAEADLVAYYCHYLSS-YTFGGGKLEIK 114
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      90  ESGVDPDRFSGSGSSTDFTLTSSLQAEADVAVYYCQQYISTPYSFGGGKLEIK 142

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Job time : 394.277 secs

Matches 99; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYWASTR 60

Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQOKPGQPKLLIYWASTR 60

QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSS-YTFGGGTKEIK 112

Db 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCQOYLTTPPTFGGTKEIK 113

RESULT 11

S51147

antibody light chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C/Accession: S51147

R/de Kruijf, J.; Boel, E.; Logtenberg, T.

submitted to the EMBL Data Library, January 1995

A/Description: Selection and application of human SCFV antibody fragments from a semi-sy

A/Reference number: S51147

A/Accession: S51147

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-120 <DEX>

A/Cross-references: EMBL:X83714; NID:G633227; PIDN:CAA56689.1; PID:G633228

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F,16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 87.0%; Score 507.5; DB 2; Length 120;

Matches 98; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYWASTR 60

Db 1 DIETQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQOKPGQPKLLIYWASTR 60

QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSS-YTFGGGTKEIK 112

Db 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCQOYSTLTWTFGGGTKEIK 113

RESULT 12

PH1054

Ig light chain V region (clone 202.135) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C/Accession: PH1054

R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1054

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-103 <TIL>

A/Experimental source: B cell, strain [N2B x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F,16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 87.0%; Score 507; DB 2; Length 103;

Matches 96; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYWASTR 60

Db 1 NIMMTQSPSLAVSAGEKVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYWASTR 60

QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSSYTF 103

Db 61 ESGVPDRFRTSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSSYTF 103

RESULT 13

S30520

Ig kappa chain V region - human

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S30520

R/Mariette, X.

submitted to the EMBL Data Library, October 1992

A/Reference number: S30520

A/Accession: S30520

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 <MAR>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F,16-96/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 86.2%; Score 502.5; DB 2; Length 113;

Matches 96; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYWASTR 60

Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQOKPGQPKLLIYWASTR 60

QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSS-YTFGGGTKEIK 112

Db 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCQOYNTPLTFGGGTKEIK 113

RESULT 14

PT0356

Ig kappa chain V region (2B1.1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000

C/Accession: PT0356

R/Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.

J. Exp. Med. 173, 287-296, 1991

A/Title: A novel class of anti-DNA antibodies identified in BALB/c mice.

A/Reference number: PT0352; MUID:91108325; PMID:1988536

A/Accession: PT0356

A/Molecule type: mRNA

A/Residues: 1-118 <SHE>

A/Experimental source: strain BALB/c

C/Note: the authors translated the codon CTT for residue 32 as Ser

C/Comment: This protein is an anti-double-stranded DNA antibody.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F,19-99/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.8%; Score 500; DB 2; Length 118;

Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYWASTR 60

Db 4 DIVMSQSPSLAVSVGEKVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLLIYWASTR 63

QY 61 ESGVPDRFSGSGSGTDFTLTITSSVQAEDLAVYYCHQYLSSYTFGGGTKEIK 112

Db 64 ESGVPDRFRTSGSGSGTDFTLTITSSVQAEDLAVYYCQOYYSYPTTFGGGTKEIK 115

RESULT 15

S44116

Ig kappa chain V-J region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C/Accession: S44116

R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

submitted to the EMBL Data Library, March 1994

A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re

A/Reference number: S44105
A/Accession: S44116
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <HAW>
A/Cross-references: EMBL:Z31391; NID:g472970; PIDN:CAA83266.1; PID:g940527
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 495.5; DB 2; length 114;
Best Local Similarity 85.0%; Pred. No. 6.3e-38;
Matches 96; Conservative 7; Mismatches 9; Indels 1; Gaps 1;
QY 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLTLYWASTR 60
1 DIVMTQSPDSLAVSLGERATINCKSSQSLYSSNNKTYLAWYQOKPGQSPKLTIKWASTR 60
DB 1 DIVMTQSPDSLAVSLGERVTMCKSSQSVLYSSNOKNYLAWYQOKPGQSPKLTLYWASTR 60
QY 61 ESGVPDRFSGSGGTDFLTITISVQAEDLAVYYCHQYLS-YTFGGGTKLEIK 112
61 ESGVPDRFSGSGGTDFLTITISVQAEDVAVFYCQGYTSPITFGGGTKVEIK 113
DB 61 ESGVPDRFSGSGGTDFLTITISVQAEDVAVFYCQGYTSPITFGGGTKVEIK 113

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Job time : 13.5177 secs